

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:07:24 ; Search time 17 Seconds
(without alignments)
1175.668 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREEDETVTVGI.....KEICDYPFRQIAKWHVLCGD 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2201	100.0	425	1	SYT4_HUMAN
2	2006	91.1	425	1	SYT4_RAT
3	1988	90.3	425	1	SYT4_MOUSE
4	1167.5	53.0	430	1	SYTB_MOUSE
5	1162	52.8	431	1	SYTB_HUMAN
6	1156.5	52.5	430	1	SYTB_RAT
7	627.5	28.5	403	1	SYT7_MOUSE
8	623.5	28.3	474	1	SY65_DROME
9	615.5	28.0	402	1	SYT7_HUMAN
10	606.5	27.6	426	1	SY65_APLCA
11	604.5	27.5	422	1	SYT2_MOUSE
12	603.5	27.4	422	1	SYT2_RAT
13	594.5	27.0	537	1	SY63_DISOM
14	594	27.0	441	1	SYT1_CAEEL
15	592	26.9	498	1	SYTA_RAT
16	590	26.8	523	1	SYTA_MOUSE
17	581	26.4	421	1	SYT1_MOUSE
18	581	26.4	422	1	SYT1_BOVIN
19	581	26.4	422	1	SYT1_HUMAN
20	580.5	26.4	386	1	SYT5_MOUSE
21	580	26.4	421	1	SYT1_RAT
22	579.5	26.3	427	1	SY61_DISOM
23	575	26.1	424	1	SYT1_CHICK
24	574.5	26.1	439	1	SY62_DISOM
25	573.5	26.1	386	1	SYT5_HUMAN
26	571.5	26.0	386	1	SYT5_MOUSE
27	520	23.6	588	1	SYT3_RAT
28	518.5	23.6	590	1	SYT3_HUMAN
29	516	23.4	587	1	SYT3_MOUSE
30	408	18.5	704	1	RP3A_BOVIN
31	399.5	18.2	694	1	RP3A_HUMAN
32	394.5	17.9	681	1	RP3A_MOUSE
33	393.5	17.9	684	1	RP3A_RAT

34	361.5	16.4	395	1	SYTB_MOUSE
35	332	15.1	1021	1	YPT7_CAEEL
36	192.5	8.7	5120	1	PCLO_CHICK
37	184.5	8.4	5147	1	PCLO_HUMAN
38	181.5	8.2	5038	1	PCLO_MOUSE
39	180	8.2	5085	1	PCLO_RAT
40	179.5	8.2	682	1	KPCG_BOVIN
41	179.5	8.2	697	1	KPCG_RABIT
42	178.5	8.1	697	1	KPCG_HUMAN
43	177.5	8.1	697	1	KPCG_MOUSE
44	175	8.0	826	1	RSGS_HUMAN
45	173.5	7.9	834	1	RSGS_BOVIN

ALIGNMENTS

RESULT 1
SYT4_HUMAN
ID SYT4_HUMAN STANDARD; PRT; 425 AA.
AC Q9H2E2; Q9P2K4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Synaptotagmin IV (SyTIV).
GN SYT4 OR KIAA1342.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20538435; PubMed=10938284;
RA Ferguson G.D., Chen X.-N., Korenberg J.R., Herschman H.R.;
RT "The human synaptotagmin IV gene defines an evolutionary break point
RT between synaptic mouse and human chromosome regions but retains
RT ligand inducibility and tissue specificity."
RL J. Biol. Chem. 275:36920-36926(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:65-73(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
CC secretory vesicles through Ca(2+) and phospholipid binding to the

P47709 rattus norv

CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
 CC vesicles.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN. WITHIN BRAIN, EXPRESSION
 CC IS HIGHEST IN HIPPOCAMPUS, WITH SUBSTANTIAL LEVELS ALSO DETECTED
 CC IN AMYGDALA AND THALAMUS.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
 CC
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 CC
 CC EMBL; AF299075; AAG37229.1; -;
 CC EMBL; AB037763; BAA92580.1; ALT_INIT.
 CC EMBL; BC036538; AAH36538.1; -;
 CC HSSP; P21707; 1BYN.
 CC Genew; HGNC:11512; SYT4.
 CC MIM; 600103; -;
 CC GO; GO:0016021; C:regulation of membrane; ISS.
 CC GO; GO:0017158; P:regulation of calcium ion dependent exocytosis; ISS.
 CC GO; GO:0016181; P:synaptic vesicle transport; ISS.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR002149; LRI.
 CC InterPro; IPR001565; Synaptotagmin.
 CC Pfam; PF00168; C2; 2.
 CC PRINTS; PR00399; SYNAPTOTAGMIN.
 CC SMART; SM00239; C2; 2.
 CC PROSITE; PS00499; C2_DOMAIN_1; 2.
 CC PROSITE; PS50004; C2_DOMAIN_2; 2.
 CC Transmembrane; Repeat; Synapse.
 CC DOMAIN 1 16 VESICULAR (POTENTIAL).
 CC TRANSMEM 17 37 POTENTIAL.
 CC DOMAIN 38 425 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 147 297 PHOSPHOLIPID BINDING (PROBABLE).
 CC DOMAIN 155 258 C2 DOMAIN 1.
 CC DOMAIN 289 392 C2 DOMAIN 2.
 CC SEQUENCE 425 AA; 47958 MW; DA3D4CB175CB528D CRC64;
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 CC Query Match 100.0%; Score 2201; DB 1; Length 425;
 CC Best Local Similarity 100.0%; Pred. No. 6.4e-145;
 CC Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 CC 1 MAPITTSREEDFDEIPTVVGIFSAFGLVFTVSLFAMICQKRSKSNKTPPKYFVHLKGV 60
 CC 1 MAPITTSREEDFDEIPTVVGIFSAFGLVFTVSLFAMICQKRSKSNKTPPKYFVHLKGV 60
 CC 61 DTYPENLNKKKFGADKKNEKNKPAVPKNSIHLDLEKRDNLNGFPKTNLKGSPSDLEN 120
 CC 61 DTYPENLNKKKFGADKKNEKNKPAVPKNSIHLDLEKRDNLNGFPKTNLKGSPSDLEN 120
 CC 121 ATPKLFLEGEKESVSPESLSKTSLSLSEKQKGLTFFSLEYNFERKAFVNNIKEARGL 180
 CC 121 ATPKLFLEGEKESVSPESLSKTSLSLSEKQKGLTFFSLEYNFERKAFVNNIKEARGL 180
 CC 181 PAMDEQSMSTSDYIKMTILPEKKHKVKTIVRLTLPAPDETFTFYGIPYTOIELALHF 240
 CC 181 PAMDEQSMSTSDYIKMTILPEKKHKVKTIVRLTLPAPDETFTFYGIPYTOIELALHF 240
 CC 241 TILSFDERSRDDIIGEVLLPLSGIELSEGKMLMNRRIKENVKSSGRGELLISLCYQST 300
 CC 241 TILSFDERSRDDIIGEVLLPLSGIELSEGKMLMNRRIKENVKSSGRGELLISLCYQST 300
 CC 301 TNLTLVVLKAHLPKSDVSGISDPYKVNKLHAKKRIISKKTHVKKCTPAVNFNLFVF 360
 CC 301 TNLTLVVLKAHLPKSDVSGISDPYKVNKLHAKKRIISKKTHVKKCTPAVNFNLFVF 360
 CC 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLAAGAGTGGEHWKEICDYPRQIAKWH 420

Db 361 DIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLAAGAGTGGEHWKEICDYPRQIAKWH 420
 QY 421 VLCDG 425
 Db 421 VLCDG 425

RESULT 2

SYT4_RAT
 ID SYT4_RAT STANDARD; PRT; 425 AA.
 AC P50232;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Synaptotagmin IV (SYTIV).
 GN SYT4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95085772; PubMed=7993622;
 RA Ullrich B., Li C., Zhang J.Z., McMahon H., Anderson R.G., Geppert M.,
 RA Suedhof T.C.;
 RT "Functional properties of multiple synaptotagmins in brain.";
 RL Neuron 13:1281-1291(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95199312; PubMed=7892240;
 RA Vician L., Lim I.K., Ferguson G., Tocco G., Baudry M., Herschman H.R.;
 RT "Synaptotagmin IV is an immediate early gene induced by
 RT depolarization in PC12 cells and in brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2164-2168(1995).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+) and phospholipid binding to the
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
 CC vesicles.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
 CC
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 CC
 CC EMBL; U14398; AAA68519.1; -;
 CC EMBL; L38247; AAA67327.1; -;
 CC PIR; I59355; I59355.
 CC HSSP; P21707; 1BYN.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0017158; P:regulation of calcium ion dependent exocytosis; ISS.
 CC GO; GO:0016181; P:synaptic vesicle transport; ISS.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR001565; Synaptotagmin.
 CC Pfam; PF00168; C2; 2.
 CC PRINTS; PR00360; C2DOMAIN.
 CC SMART; SM00239; SYNAPTOTAGMIN.
 CC PROSITE; PS00499; C2_DOMAIN_1; 2.
 CC PROSITE; PS50004; C2_DOMAIN_2; 2.
 CC Transmembrane; Repeat; Synapse.
 CC DOMAIN 1 16 VESICULAR (POTENTIAL).
 CC TRANSMEM 17 37 POTENTIAL.
 CC DOMAIN 38 425 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 147 297 PHOSPHOLIPID BINDING (PROBABLE).
FT DOMAIN 155 258 C2 DOMAIN 1.
FT DOMAIN 289 392 C2 DOMAIN 2.
SQ SEQUENCE 425 AA; 47685 MW; 6AC88E0878936BB CRC64;

Query Match
Best Local Similarity 91.1%; Score 2006; DB 1; Length 425;
Matches 382; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLFAMICCCORRKSNSKNTPPYKPVHVLKGV 60
Db 1 MAPITTSRVEFDEIPTVVGIFSAFGLVFTVSLFAMICCCORRKSNSKNTPPYKPVHVLKGV 60

QY 61 DIYPENLNKKFGADDKNEVKNKPAVKNSLHLDLEKRDINGNFPKTNLKPSPSPLEN 120
Db 61 DIYPENLNSSQKFGDDKSEVKGKTALPNLSLHLDLEKRDINGNFPKTNLKPSPSPLEN 120

QY 121 ATPKLFLEGEKESVPSLSKSTSLTSEKQKGLTLPFSLYNNPERKAFVNNIKEARGL 180
Db 121 VTPKLFPETEKEAVSPSLKSTSLTSEKQKGLTLPFSLYNNPERKAFVNNIKEARGL 180

QY 181 PAMDEQSMTSDPYIKMTILPEKKHKVKTIVLAKTLDPAFDEFTFYGIPYTOIELALHF 240
Db 181 PAMDEQSMTSDPYIKMTILPEKKHKVKTIVLAKTLDPAFDEFTFYGIPYTOIELALHF 240

QY 241 TILSFDRFSRDDIIGEVILPLSGIELSGKMLMREIIRKNNVNRKSGRGELLISLCYQST 300
Db 241 TILSFDRFSRDDIIGEVILPLSGIELSGKMLMREIIRKNNVNRKSGRGELLISLCYQST 300

QY 301 TNLTVVVLKARHLPKSDVSGLSGSDPYVKNLYHAKRKISKKTHVKKCTPNVFNELFVF 360
Db 301 TNLTVVVLKARHLPKSDVSGLSGSDPYVKNLYHAKRKISKKTHVKKCTPNVFNELFVF 360

QY 361 DIPCEGLIEDISVEFLVLDSEGRSNEVIGQLVGAAGTGGGEHWKEICDYPRROIATKWH 420
Db 361 DIPCEGLEEISVEFLVLDSEGRSNEVIGRLVLGATAGSGGGHKEICDFPRROIATKWH 420

QY 421 VLCDG 425
Db 421 MLCDG 425

RESULT 3
SYTH4 MOUSE
ID SYTH4 MOUSE STANDARD; PRT; 425 AA.
AC P40749;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Synaptotagmin IV (SytIV).
GN SYTH4 OR SYTH3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=94336712; PubMed=8058779;
RT Hilbush B.S., Morgan J.I.;
RL "A third synaptotagmin gene, Syt3, in the mouse.";
CC Proc. Natl. Acad. Sci. U.S.A. 91:8195-8199 (1994).
CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
CC secretory vesicles through Ca(2+) and phospholipid binding to the
CC C2 domain or may serve as Ca(2+) sensors in the process of
CC vesicular trafficking and exocytosis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Synaptic
CC vesicles.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY REGIONS OF THE NERVOUS
CC SYSTEM BUT IS UNDETECTABLE IN EXTRA NEURAL TISSUES.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.

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EMBL; U10355; AAA20971.1; -.
DR HSSP; P21707; 1BYN.
DR MGD; MGI:101759; SYL4.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0017158; P:regulation of calcium ion dependent exocytosis; TAS.
DR GO; GO:0016181; P:synaptic vesicle transport; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR InterPro; IPR001565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00399; SYNAPTOTAGMN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00499; C2 DOMAIN 1; 2.
DR PROSITE; PS50004; C2 DOMAIN 2; 2.
DR Transmembrane; Repeat; Synapse.
KW DOMAIN 1 16 VESICULAR (POTENTIAL).
FT TRANSMEM 17 37 POTENTIAL.
FT DOMAIN 38 425 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 147 297 PHOSPHOLIPID BINDING (PROBABLE).
FT DOMAIN 155 258 C2 DOMAIN 1.
FT DOMAIN 289 392 C2 DOMAIN 2.
SQ SEQUENCE 425 AA; 47630 MW; D1900D475C163821 CRC64;

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Query Match 90.3%; Score 1988; DB 1; Length 425;
 Best Local Similarity 89.4%; Pred. No. 3.3e-130;
 Matches 380; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

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QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLFAMICCCORRKSNSKNTPPYKPVHVLKGV 60
Db 1 MAPITTSRVEFDEIPTVVGIFSAFGLVFTVSLFAMICCCORRKSNSKNTPPYKPVHVLKGV 60

QY 61 DIYPENLNKKFGADDKNEVKNKPAVKNSLHLDLEKRDINGNFPKTNLKPSPSPLEN 120
Db 61 DIYPENLNSSQKFGDDKSEVKGKTALPNLSLHLDLEKRDINGNFPKTNLKPSPSPLEN 120

QY 121 ATPKLFLEGEKESVPSLSKSTSLTSEKQKGLTLPFSLYNNPERKAFVNNIKEARGL 180
Db 121 VTPKLFPETEKEANSVPSLSKSTSLTSEKQKGLTLPFSLYNNPERKAFVNNIKEARGL 180

QY 181 PAMDEQSMTSDPYIKMTILPEKKHKVKTIVLAKTLDPAFDEFTFYGIPYTOIELALHF 240
Db 181 PAMDEQSMTSDPYIKMTILPEKKHKVKTIVLAKTLDPAFDEFTFYGIPYTOIELALHF 240

QY 241 TILSFDRFSRDDIIGEVILPLSGIELSGKMLMREIIRKNNVNRKSGRGELLISLCYQST 300
Db 241 TILSFDRFSRDDIIGEVILPLSGIELSGKMLMREIIRKNNVNRKSGRGELLISLCYQST 300

QY 301 TNLTVVVLKARHLPKSDVSGLSGSDPYVKNLYHAKRKISKKTHVKKCTPNVFNELFVF 360
Db 301 TNLTVVVLKARHLPKSDVSGLSGSDPYVKNLYHAKRKISKKTHVKKCTPNVFNELFVF 360

QY 361 DIPCEGLIEDISVEFLVLDSEGRSNEVIGQLVGAAGTGGGEHWKEICDYPRROIATKWH 420
Db 361 DIPCEGLEEISVEFLVLDSEGRSNEVIGRLVLGATAGSGGGHKEICDFPRROIATKWH 420

QY 421 VLCDG 425
Db 421 MLCDG 425

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RESULT 4
 SYTH4 MOUSE
 ID SYTH4 MOUSE STANDARD; PRT; 430 AA.
 AC Q9R0N3;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Synaptotagmin XI (SytXI).
 GN SYT11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Cerebellum;
 RX MEDLINE=20002669; PubMed=10531343;
 RA Fukuda M., Kanno E., Mikoshiba K.;
 RT "Conserved N-terminal cysteine motif is essential for homo- and
 RT heterodimer formation of synaptotagmins III, V, VI, and X.";
 RL J. Biol. Chem. 274:31421-31427(1999).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+) and phospholipid binding to the
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis (By similarity).
 CC -!- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
 CC VESICLES (By similarity).
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
 CC
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 CC
 CC -----
 CC EMBL: AB026808; BAA85780.1; --
 CC HSSP: P21707; IRSY.
 CC MGD: MGI:1859547; Syt11.
 CC GO: GO:0005887; C:integral to plasma membrane; IDA.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002149; LRI.
 CC InterPro: IPR001565; Synaptotagmin.
 CC Pfam: PF00168; C2; 2.
 CC PRINTS: PR00399; SYNAPTOTAGMIN.
 CC SMART: SM00239; C2; 2.
 CC PROSITE: PS00499; C2 DOMAIN 1; FALSE_NEG.
 CC PROSITE: PS50004; C2 DOMAIN 2; 2.
 CC Transmembrane, Repeat; Synapse.
 CC DOMAIN 1 15 VESICULAR (POTENTIAL).
 CC TRANSMEM 16 36 POTENTIAL.
 CC DOMAIN 37 430 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 173 261 C2 DOMAIN 1.
 CC DOMAIN 303 396 C2 DOMAIN 2.
 CC SEQUENCE 430 AA; 48359 MW; 25E7CDFC4B4BE036 CRC64;
 Query Match 53.0%; Score 1167.5; DB 1; Length 430;
 Best Local Similarity 51.0%; Pred. No. 1.7e-73;
 Matches 233; Conservative 70; Mismatches 93; Indels 61; Gaps 8;
 Qy 1 MAPITTSREDFEIPVVGIFSAFLGVLFTVS--LFAWICQKSSKSNKTPPYKVFHVLK 58
 Db 1 MAEITNRPSPDVSFVAAAGLIGASLVVCSVTVFVWTCCHQAEKKGKTPPYKFIHMLK 60
 Qy 59 GVDIIPENLNSKKK-----FGADDKNEVKNKPAVPKNS 91
 Db 61 GISIYPETLSNKKKIIVKRDKDPRESGRGNLLINAEISGLLSHDKDPRGSPSPASCDQ 120
 Qy 92 LHLDLKSLDNGNF--PKTNLPKGSFDLENATPKLFLEGEKESVSPESLKSSTLSLTSSE 149
 Db 121 LPI-----KRDYGBELSPMTSLTP-----GESKPTSP-----SSPE 152
 Qy 150 KOEKLGLTFFSLEYNFERKAFVNVNIKEARGLPAMDQSMTSDFYIKMTILPEKKHKVYKTR 209

Db 153 EDVMLGSLTFSVDYVNFPAKALVVTIQEAHGLPVMDDQQTGSDPYIKMTILPKRHRVYKTR 212
 Qy 210 VLKRTLPADFETFTFYGIPTQIQELAHFTILSFDFRSRDDIIGEVILPLSGIELSEG 269
 Db 213 VLKRTLPVDFETFTFYGIPYSQQLDLVHLVLSFDFRSRDDVIGEVVPLAGVDSTG 272
 Qy 270 KMLMREIIRKVRKSGRGELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLS-DFYVK 328
 Db 273 KVQLTRDIIRKNIQKICSRGELQVSLSYQVAQRMTVVVVKARHLPKMDITGLSGNPYVK 332
 Qy 329 VNLVHAKKRISKKTHVKKCTPNAFVNFELVFDIPCEGLEDSLEVLVLDSEGRSNEVI 388
 Db 333 VNVYGRKRIAKKTHVKKCTLPNPFNBSFVPTDILLPDISIEFLVDFDRTTKNEV 392
 Qy 389 GQLVLGAAGTGT-GGEHWKEICDYPKQIAKWHVLC 424
 Db 393 GRLLIGHSVTTSAGHREVCESPKPIAKWHLSLSE 429
 RESULT 5
 SYTB HUMAN STANDARD; PRT; 431 AA.
 AC Q9BT88;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Synaptotagmin XI (SytXI).
 GN SYT11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isozaki T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
 CC secretory vesicles through Ca(2+) and phospholipid binding to the
 CC C2 domain or may serve as Ca(2+) sensors in the process of
 CC vesicular trafficking and exocytosis (By similarity).
 CC -!- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
 CC VESICLES (By similarity).
 CC -!- SIMILARITY: Contains 2 C2 domains.

```

CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AK074931; BAC11300.1; -
CC EMBL; BC004291; AA04291.1; -
CC EMBL; BC013690; AAH13690.1; -
CC HSSP; P21707; IRSY.
CC Genew; HGNC:19239; SYT11.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; SM00239; C2; 2.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
CC PROSITE; PS00004; C2_DOMAIN_2; 2.
CC Transmembrane; Repeat; Synapse.
CC KW DOMAIN 1 15 VESICULAR (POTENTIAL).
CC FT TRANSMEM 16 36
CC FT DOMAIN 37 431 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 174 262 C2 DOMAIN 1.
CC FT DOMAIN 304 397 C2 DOMAIN 2.
CC SQ SEQUENCE 431 AA; 48306 MW; A7F76AD745COFF7D CRC64;

Query Match 52.8%; Score 1162; DB 1; Length 431;
Best Local Similarity 52.4%; Pred. No. 4e-73;
Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

QY 1 MAPITTSREDFEIPITVVGIFSAFGLVFTVS--LPAWICCOCKSKSKNTPPYKPVHLK 58
Db 1 MAEITNIRPSFDVSPVVAAGLIGASVLVVCVSVTVFVMSCHQQAQKHKTPPYKTHMLK 60

QY 59 GVDIYPENLNSKKKFGADDKNEVKNKPAVKNLSHLDLK-----RLNGNFP----- 106
Db 61 GSIIYETLSNKKKIIKVRDKDQSGHRESGRNLLVNAESGLLSHDDPRGSPASCIQ 120

QY 107 ---KTNLKPSPSDLENATPKLFLGEGESVSPESLSSTSLTSEEKGLTLPFFSLEY 163
Db 121 LPIKRDYGEELRSPMTSLTP-----GESKTSF-----SSPEEDVMLGSLTFSDY 166

QY 164 NFERKAFVYNIKEARGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLRKTLDPAFDETF 223
Db 167 NFPKKALVVTIQEAHGLPVMDDGTQSDPYIKMTILPKRHRVTRVLRKTLDPVFEDETF 226

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Synaptotagmin XI (SYTXI).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97306341; PubMed=9162066;
RA von Poser C., Ichtchenko K., Shao X., Rizo J., Suedhof T.C.;
RT "The evolutionary pressure to inactivate. A subclass of synaptotagmins
RL J. Biol. Chem. 272:14314-14319(1997).
CC -1- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
CC secretory vesicles through Ca(2+)- and phospholipid binding to the
CC C2 domain or may serve as Ca(2+) sensors in the process of
CC vesicular trafficking and exocytosis (By similarity).
CC -1- SUBUNIT: Homodimer. Can also form heterodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
CC VESICLES (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in brain and at lower levels
CC in other tissues.
CC -1- SIMILARITY: Contains 2 C2 domains.
CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF000423; AAB58344.1; -
CC HSSP; P21707; IRSY.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; PR00399; SYNAPTOTAGMIN.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
CC PROSITE; PS00004; C2_DOMAIN_2; 2.
CC Transmembrane; Repeat; Synapse.
CC KW DOMAIN 1 15 VESICULAR (POTENTIAL).
CC FT TRANSMEM 16 36
CC FT DOMAIN 37 430 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 158 261 C2 DOMAIN 1.
CC FT DOMAIN 292 396 C2 DOMAIN 2.
CC SQ SEQUENCE 430 AA; 48268 MW; C1FA13CB9177C825 CRC64;

Query Match 52.5%; Score 1156.5; DB 1; Length 430;
Best Local Similarity 51.5%; Pred. No. 9.6e-73;
Matches 228; Conservative 78; Mismatches 104; Indels 33; Gaps 7;

QY 1 MAPITTSREDFEIPITVVGIFSAFGLVFTVS--LPAWICCOCKSKSKNTPPYKPVHLK 58
Db 1 MAEITNIRPSFDVSPVVAAGLIGASVLVVCVSVTVFVMSCHQQAQKHKTPPYKTHMLK 60

QY 59 GVDIYPENLNSKKKFGADDKNEVKNKPAVKNLSHLDLK-----RLNGNFP----- 106
Db 61 GSIIYETLSNKKKIIKVRDKDQSGHRESGRNLLVNAESGLLSHDDPRGSPASCIQ 120

QY 107 ---KTNLKPSPSDLENATPKLFLGEGESVSPESLSSTSLTSEEKGLTLPFFSLEY 163
Db 121 LPIKRDYGEELRSPMTSLTP-----GESKTSF-----SSPEEDVMLGSLTFSDY 166

QY 164 NFERKAFVYNIKEARGLPAMDQSMSTDPYIKMTILPEKKHKVTRVLRKTLDPAFDETF 223
Db 167 NFPKKALVVTIQEAHGLPVMDDGTQSDPYIKMTILPKRHRVTRVLRKTLDPVFEDETF 226

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RESULT 6
 SYTB RAT
 ID SYTB RAT
 AC O08835;
 DT 16-OCT-2001 (Rel. 40, Created)

Qy	224	TFYGIPTQIQELALHFTLSPD	FRSDRIIGEVLPISG	ISLGKMLMREII	KNRV	283
Db	227	TFYGIPTQIQELALHFTLSPD	FRSDRIIGEVLPISG	ISLGKMLMREII	KNRV	286
Qy	284	KSSRGELLISLCYOSTNTLT	VVVLKARHLPKSDV	SGLS-DPYKVN	IYHAKGISKKK	342
Db	287	KCISRGELQVLSLQPVQ	QRMTVVVLKARHLPKMDIT	GLSGNPPYKVN	YVYGRKIAKKK	346
Qy	343	THVKKCTPNVAFNELF	PDIECEGLDTSVEFLVD	SRGSRNEVI	IGQLGAAAGT-G	401
Db	347	THVKKCTLPINFES	DIYDITDLLPDISL	BEFLVDFTKNE	VVGRILGAHSTSG	406
Qy	402	GEHWKEICDYP	RRQIAKWHV	LCDD		424
Db	407	AEHWREVCES	PRKPKVAKHSL	SE		429

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RESULT 7
SYT7_MOUSE
ID SYT7_MOUSE STANDARD; PRT; 403 AA.
AC Q9R0N7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Synaptotagmin VII (SytVII).
GN SYT7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=ICR; TISSUE=Cerebellum;
RC MEDLINE=20002669; PubMed=10531343;
RX Fukuda M., Kanno E., Mikoshiba K.;
RT "Conserved N-terminal cysteine motif is essential for homo- and
RT heterodimer formation of synaptotagmins III, V, VI, and X.";
RL J. Biol. Chem. 274:31421-31427(1999).
CC -!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
CC secretory vesicles through Ca(2+) and phospholipid binding to the
CC C2 domain or may serve as Ca(2+) sensors in the process of
CC vesicular trafficking and exocytosis (By similarity).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
CC VESICLES (By similarity).
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.

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CC	EMBL; AB026804; BAA85776.1; --
CC	HSSP; P21707; IRSY.
DR	MGI; MGI:1859545; Syt7.
DR	InterPro; IPR000008; C2.
DR	InterPro; IPR002149; LRI.
DR	InterPro; IPR001565; Synaptotagmin.
DR	Fram; PF00168; C2; 2.
DR	PRINTS; PR00360; C2DOMAIN.
DR	PRINTS; PR00399; SYNAPTOTAGMN.
DR	PROSITE; PS00499; C2.DOMAIN.1; 2.
DR	PROSITE; PS50004; C2.DOMAIN.2; 2.
KW	Transmembrane; Repeat; Synapse.
FT	DOMAIN 1 16 VESICULAR (POTENTIAL).
FT	TRANSMEM 17 37 POTENTIAL.
FT	DOMAIN 38 403 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 137 239 C2 DOMAIN 1.
FT	DOMAIN 268 371 C2 DOMAIN 2.

```

SQ SEQUENCE 403 AA; 45472 MW; 4E63C5C779C2ED43E CRC64;

Query Match
Best Local Similarity 36.2%; Score 627.5; DB 1; Length 403;
Matches 153; Conservative 71; Mismatches 128; Indels 71; Gaps 11;

QY 27 VFTVSL-----FAWIC--CORKSSKGNKTPPYKFVHVHLKGVDIYPENLSKKKFGADD-- 77
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 23 IITVSLSVTIVLCGLCHWCQKLGKRYK-----NSLETGVTGTPDSG 62

QY 78 -----KNEVK-----NKPAPVKNSLHLDLKRDLDNGNFPKTNLKGSPSDLDENATPK 124
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 63 RGRGSKKAIKLPAGKAVNATPVPGTQPHDESDR-----TETR--SSVSDLVN----- 109

QY 125 LFLEGEKESVSPESLSKSTSLTSEE-----KQEKLGTLFFSLEYNFERKAFVNNKEARG 179
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 110 -----SLTSEMLSPGSEDEAHEGCSRENLRGQISGVGNFQBSTITVVKYMAQE 161

QY 180 LPAMDEQSMTSDPYIKMTILPEKKHKVKTURLKTLDPADFDETFTFYGIPYTOIELAH 239
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 162 LPKD--FSGTSDPFVKIYLLDPKKHLEIKVKEKNLPHNNETLFEFGFPEKVVQRVLY 220

QY 240 FTILSDFRPSDDITGEVLPIPSGIELSEGMIMNREIIRKNVRKSSGRGELLISLCYQS 299
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 221 LQVLDYDFRSDNDPICEVSIPLNKVDLTQ--MQTFWKDLKPCSDGSGRSELLSLCYNP 278

QY 300 TTNTLTVVVLKARHLPKSDVSLGSPYKVNLYHAKRISKKKTHVVKCTPNVAFNELPV 359
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 279 SANSIIIVNIIKARNLKAMDIGTSGPYVKVWLMYKDKRKVEKKKTVTTKRNLNLPFNESFA 338

QY 360 FDIFCEGLIEDISVEPLVDLSERGSRNEVIGQLVGAAGCTGGEHWKEICDYPRRQIAKW 419
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 339 EDIPEKLEWETIIITVMDKDKLSRNDVLGKIYLSWKSGBGEVKHKMDIARPPQVAQW 398

QY 420 HVL 422

Db 399 HOL 401

```

RESULT 8

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RESUL-8
SY65_DROME
ID SY65_DROME STANDARD; PRT; 474 AA.
AC P21521;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Synaptotagmin (p65).
GN SYT.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91093190; PubMed=1840599;
RA Perin M.S.; Johnston P.A.; Oezcelik T.; Jahn R.; Francke U.,
RA Suedhof T.C.;
RT "Structural and functional conservation of synaptotagmin (p65) in
RT Drosophila and humans."
RL J. Biol. Chem. 266:615-622(1991).
CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE.
CC -!- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
CC -!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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Qy	180	LPAMDEQSWTSDPYIKMTILPEKHKHKVTRVLKRTILDPAFDEFTFYGIPYQIOELALH	239
Db	161	LPKAD-FSGTSDPFVKIYLLPKXHKLKTKVKRKNLPHWNTEFLFEGFPYKVVQRIY	219
Qy	240	FTILSFDFSRDDIIGEVLIPLSGLESECKMLMNPRIIKRNVKSGSGGELLISCTQS	299
Db	220	LQVLDYDFSRNDPGEVSIPLUNKVDLTQ--MOTFWKOLPCSDSGSGGELLISLCYNP	277
Qy	300	TNTNLTVVVLKARHLPKSDVSLSDPYVKVNIYHAKRKISKKTKHVKCTPNVNEULFV	359
Db	278	SANSTIIVNIKARNLKAMDIGTSDPYVKVLMYKDKRVEKKCTVTMKNLNPNESFA	337
Qy	360	FDIPCEGEDLSVEPLVLDSESGSNVEVIGQVLGAABEGTGGETHKEICDYPRIQIAKW	419
Db	338	FDITEKLRETIIITVMDKOKLSRNDVIGKTYLSWKSGPGGEVXHWKOMIARPROPVAQW	397
Qy	420	HVL	422
Db	398	HQL	400

```

RESULT 10
SY65 APLCA
ID -SY65 APLCA STANDARD; PRT; 426 AA.
AC P41823;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Synaptotagmin [p65].
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OC NCBI_TaxID=6500;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Ganglion;
RA Hu Y.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
CC STRUCTURES.
CC -1- SIMILARITY: Contains 2 C2 domains.
CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcements
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U03125; AAA03567.1; --
CC HSPSP; P21707; IRSY.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; PR00360; C2DOMAIN.
CC PRINTS; PR00399; SYNAPTOTAGM.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN_1; 2.
CC PROSITE; PSS0004; C2_DOMAIN_2; 2.
CC Transmembrane; Repeat; Synapse; Glycoprotein.
CC DOMAIN 1 67 VESICULAR (POTENTIAL).
CC FT TRANSMEM 67 92
CC FT DOMAIN 93 426 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 145 393 PHOSPHOLIPID BINDING (PROBABLE)
CC

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QY	10	ERDEIP----	TVVGIFSAGLIVTSLFA--	WTCCORSSKSNKTPPYKFVHVLUKGVDI	62
Db	57	ENIKPIPPWALITAMAVVAGLLLTCCFCIKKCCCKKKNNKKKG----	KGM--	105	

QY 63 YPENLNSKKFGADDKNEVKNKPAVPKNSLHLDLEKRLNGNFKTNLKPSPSLENAT 122
 Db 106 -KNAMNMKMGQDDDDA-----ETGLTEG----- 130
 QY 123 PKLFLGEKESVSPESLKSSLTSEKQKGLTLFFSLEYNFKKAPVVKKEARGLPA 182
 Db 131 -----EGEGE-----EKEPENLGLQSLDVFQANQUTVGVLOAELPA 171
 QY 183 MDEQSWTSDPYIKMTILPEKHKHKTAVLRTLPAPDETFTFYGYPTQIQELALHFTI 242
 Db 172 LD-MGTSDDPYKVFLLPDKKKYETKVKHTLNPANFNFTF-KVPQELGGKTLWAI 229
 QY 243 LSFDFRSRDDIIGEVLLPLSGIEL-----SEKMLMNPBIIKRVKSGRGELISICYQ 298
 Db 230 YDFDFRSKDDIIGEVKVPMTVDLQGOIEWRDLQGE--KEEPEK--LGDICTSLRYV 284
 QY 299 STTNLTIVVVLKARHLPKSDVGLSDPYKVNLYHAKKRISKKTHVKKCTPNVAVNELF 358
 Db 285 PTAGKLTVCILEAKNLKMDVGLSDPYKVIHLMONGKRLKKKKTIVKKTLNPFNFSF 344
 QY 359 VFDICEGLEDISVFLVLDSEKSGRNEVIGQVLGAAAEGTGGEHWKEICDYPRLQIAK 418
 Db 345 SFEIPFEQIQKVVVTVLDYDKLGNKNEALGKIFVGSNATGTELRHWSMLANPRRPIAQ 404
 QY 419 WHVL 422
 Db 405 WHSL 408

RESULT 13

SY63_DISOM STANDARD; PRT; 537 AA.
 AC P24507;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Synaptotagmin C (Synaptic vesicle protein O-p65-C).
 GN P65-C.
 OS Discopyle ommata (Electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalea; Hypnosqualea; Pristiorajae; Batoidae;
 OC Torpediniformes; Narcinoidae; Narcinidae; Discopyle.
 OX NCBI_TaxID=7785;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91273991; PubMed=2054189;
 RA Wandland B., Miller K.G., Schilling J., Scheller R.H.;
 RT "Differential expression of the p65 gene family."
 RL Neuron 6:993-1007(1991).
 CC -1- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
 CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
 CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
 CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
 CC BACKBONE.
 CC -1- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
 CC -1- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
 CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----

EMBL; M64277; AAA49229.1; -.
 DR FIR; JH0415; JH0415.
 DR HSSP; P21707; IRSY.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002149; LRI.

DR InterPro; IPR001565; Synaptotagmin.
 DR Pfam; PF00168; C2; 2.
 DR PRINTS; PR00360; C2DOMAIN
 DR PRINTS; PR00399; SYNAPTOTAGMN.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS00499; C2_DOMAIN_1; 2.
 DR PROSITE; PS00504; C2_DOMAIN_2; 2.
 KW Transmembrane; Repeat; Synapse; Multigene family.
 FT DOMAIN 1 52 VESICULAR (POTENTIAL).
 FT TRANSMEM 53 78 POTENTIAL.
 FT DOMAIN 79 537 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 228 477 PHOSPHOLIPID BINDING (PROBABLE).
 FT DOMAIN 252 339 C2 DOMAIN 1.
 FT DOMAIN 382 473 C2 DOMAIN 2.
 SQ SEQUENCE 537 AA; 61300 MW; 2792F910CFBCE682 CRC64;
 Query Match 27.0%; Score 594.5; DB 1; Length 537;
 Best Local Similarity 31.5%; Pred. No. 8.7e-34;
 Matches 156; Conservative 88; Mismatches 140; Indels 111; Gaps 19;
 QY 6 TSRESEFDEIPTVVGIFSPAP-GLVFT-VSLF-AWTC-----QRKSKSKNKTTPY 51
 Db 46 TRHETDISVLSVITVFCGIVLLGVSLFVSKLWIPWRDKGLNQRDSQH---PH 102
 QY 52 KPVH-----VLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRLN 102
 Db 103 QHLHHHSHFTDLTVERVDCGP-----MPERS-YLDLE----- 135
 QY 103 GNFPKTNLK-----PGSPSDL-----EN-----A 121
 Db 136 -SYPSGIGKLSQTSPIPVDTSSGSKENNIPNAHSQQVSPAPPATFNSLPRTPOOLS 194
 QY 122 TPKLFLGEKE-----SVSPESLKSSLTSEEKQEL--GTLFFSLEYNFKKAPV 171
 Db 195 SPEFGTQADEKVEQVTSIGIKPELYKQSIDTEAKGHQKVCGRINFMLRYTTTEQLV 254
 QY 172 VNKEARGLPAMDEQSMSTSDPYIKMTILPEKHKHKTAVLRTLPAPDETFTFYGYPT 231
 Db 255 VKILKALDLPKANGF--SDPYVKIYLLPDRKKKQTKVHKTLNPIFNFTFQF-NVFPN 312
 QY 232 QIQELALHFTILSPDRFSRDDIIGEVLP--LSGIELSEKMLMNPBIIKRVKSGRG 289
 Db 313 ELQNRKHLFSVDFRFRSRHDLIGQVLDNLLEFSDFSEDFTTW-RDILEATSEKAD-LG 370
 QY 290 ELLISLCYQSTNTLTIVVVLKARHLPKSDVGLSDPYKVNLYHAKKRISKKTHVKKCT 349
 Db 371 EINFSLCYLPTAGRLTITIIKATNLKAMDLTGSDPYVKASLDCDERRLKKRTSIKNT 430
 QY 350 PNAYFNELVFDPICEGLEDISVEFLVLDSEKSGRNEVIGQVLGAAAEGTGGEHWKEIC 409
 Db 431 LNPVYNEALVFDPENNMENHVNVIIAVMDYDCIGHNEVIGMCRVGNATDGPGRHWNEML 490
 QY 410 DYPERQIAKHWVLC 424
 Db 491 ANPKRPIEQWHQLIE 505
 RESULT 14
 SYTL_CABEL STANDARD; PRT; 441 AA.
 ID SYTL_CABEL
 AC P34693;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Synaptotagmin I.
 GN SNT-1 OR F3IE8.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;

```

RX MEDLINE=93313960; PubMed=8391930;
RA Nonet M.L., Grundahl K., Meyer B.J., Rand J.B.;
RT "Synaptic function is impaired but not eliminated in C. elegans
RL mutants lacking synaptotagmin.";
RN Cell 73:1291-1305(1993).
RP
RQ SEQUENCE FROM N.A.
RA Du Z.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
CC STRUCTURES.
CC -!- TISSUE SPECIFICITY: LOCALIZED TO REGIONS KNOWN TO BE RICH IN
CC SYNAPSES AND APPEARS TO BE ASSOCIATED WITH SYNAPTIC VESICLES.
CC ALSO FOUND IN SOME NONNEURONAL SECRETORY STRUCTURES.
CC -!- DISEASE: MUTANTS EXHIBIT SEVERE BEHAVIORAL ABNORMALITIES THAT ARE
CC CHARACTERISTIC OF DEFICIENCIES IN SYNAPTIC FUNCTION, INCLUDING
CC SEVERE LOCOMOTION, FEEDING, AND DEFECTION DEFECTS.
CC -!- SIMILARITY: Contains 2 C2 domains.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L15302; AAA28145.1; -;
CC EMBL; U55856; AAA98023.1; -;
CC PIR; A40707; A40707.
CC HSSP; P21707; IRSY.
CC WormPep; F31E8.2; CE02711.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002149; LRI.
CC InterPro; IPR001565; Synaptotagmin.
CC Pfam; PF00168; C2; 2.
CC PRINTS; PR00360; C2DOMAIN.
CC PRINTS; PR00399; SYNAPTOTAGMN.
CC SMART; SM00239; C2; 2.
CC PROSITE; PS00499; C2_DOMAIN_1; 2.
CC PROSITE; PS50004; C2_DOMAIN_2; 2.
CC Transmembrane; Repeat; Synapse; Glycoprotein.
KW DOMAIN 1 69 VESICULAR (POTENTIAL).
FT TRANSMEM 70 96 POTENTIAL.
FT DOMAIN 97 441 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 175 262 C2 DOMAIN 1.
FT DOMAIN 306 397 C2 DOMAIN 2.
SQ SEQUENCE 441 AA; 49904 MW; F8D174337EB472DB CRC64;

Query Match 27.0%; Score 594; DB 1; Length 441;
Best Local Similarity 40.2%; Pred. No. 7.2e-34;
Matches 148; Conservative 57; Mismatches 111; Indels 52; Gaps 14;

QY 70 KKKEGADDKNEVKNKPAVPKNSLHLDLEKRDINGNPK-----TNLKPGSPSDLENAT 122
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
97 RKLFGKKRHE-KNK-----KGLKGFPGKGDVVDGKNIQ-GMAQDLELG 141

QY 123 PKLFLGEGKESVPSLSKSTSLTSEKQE-KLGLTFFSLEYNFERKAFVNIKEARGLP 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
142 DAM-EQNEKEQ-----AEEKEVKLCRIQYKLDYDFQQQLVTVTIQADLP 187

QY 182 AMEQSMTSDPYIKMTILPEKKHKVKTIRLKTLPADFETFTFYGIPYQIQELALHFT 241
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
188 GMD-MSGTSDPYKLYLLPEKKKKVETKVRKTLNPFVETFLP-KVAFNEITAKTILVFA 245

QY 242 ILSDFRSDRDIIIEVLIPLSGIEISGKMLMNRRI-----KRNVRKSSRGELLISLC 296

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Db	246	IYDFRSKHQJGCVLIPGKIDL--GAVIEEWKDIAPPPDKAEAKS--LGDICFSILR	301
Qy	297	YQSTNTLTIVVLKARHLPKSDVGLSDPYVKVNLVHAKKRIKKKTHVKKCTPNVAVNE	356
Db	302	YVPTAGKLTIVILEAKNLKQMDVGLSDPYKIVLMGGKKLKKKTSIKKCTLNPPYNE	361
Qy	357	LFVFDIPCEGLIEDISVFLVLDSEGRSRNEVIGLVGAAAGTGGE--HWKEICDYPRR	414
Db	362	SFSEVPFEQIQKVSILMITVMDYDKLGSNDAIGRCLLG--CNGTGAELRHWMMLASPRR	419
Qy	415	QIAKWHVL 422	
Db	420	PIAQWHTL 427	
RESULT 15			
ID	SYTA	RAT	
ID	SYTA	RAT	
AC	008625;	STANDARD;	PRT; 498 AA.
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Synaptotagmin X (SytX) (Fragment).		
GN	Syt10.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI	TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley;		
RX	MEDLINE=97226006; PubMed=9122248;		
RA	Babity J.M., Armstrong J.N., Plumier J.C., Currie R.W.,		
RA	Robertson H.A.;		
RT	"A novel seizure-induced synaptotagmin gene identified by differential display."		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:2638-2641(1997).		
CC	- - FUNCTION: May be involved in Ca(2+)-dependent exocytosis of secretory vesicles through Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis (By similarity).		
CC	- - SUBUNIT: Homodimer. Can also form heterodimer (By similarity).		
CC	- - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC VESICLES (By similarity).		
CC	- - SIMILARITY: Contains 2 C2 domains.		
CC	- - SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.		
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CC	EMBL; U85513; AAB51686.1; -		
DR	PIR; PC6300; PC6300.		
DR	HSP; P21707; IBYX.		
DR	InterPro; IPR000008; C2.		
DR	InterPro; IPR002149; LRI.		
DR	InterPro; IPR001565; Synaptotagmin.		
DR	Pfam; PF00168; C2; 2.		
DR	PRINTS; PR00360; C2DOMAIN.		
DR	PRINTS; PR00399; SYNAPTOTAGMN.		
DR	SMART; SM00239; C2; 2.		
DR	PROSITE; PS00499; C2 DOMAIN 1; 2.		
DR	PROSITE; PS00004; C2 DOMAIN 2; 2.		
DR	Transmembrane; Repeat; Synapse.		
DR	DOMAIN 1 55		
DR	VESICULAR (POTENTIAL).		
FT	TRANSMEM	56	76
FT	POTENTIAL.		
DOMAIN	77	>498	
FT	CYTOPLASMIC (POTENTIAL).		
DOMAIN	233	334	
FT	C2 DOMAIN 1		

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FT DOMAIN 365 468 C2 DOMAIN 2.
FT NON_TER 498
SQ SEQUENCE 498 AA; 56411 MW; 620BD7CD372057DE CRC64;

Query Match      26.9%; Score 592; DB 1; Length 498;
Best Local Similarity 34.6%; Pred. No. 1.2e-33;
Matches 158; Conservative 72; Mismatches 156; Indels 70; Gaps 16;

QY 20 IFSAGL-VFTVSLFA-WICQKSKSKNTPPKVHVHLKGVDIYPENLMS--KKKGA 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 DDKNEV-KKPAVPKNSLHLDLKRDLNGFP---KTNLK-----PGSPS 116
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 EEKEVEENEKEPAK-AIEPAIKSHISPDIPAEVQTAKEHLKHARVQQTDTPTSS 169
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 -----DLENATPKLFLGKES-----VSPESLKSSTLTSE----EK 150
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 170 RHNSFRHLPRQNVSSVDFSMGTPEVLRGETRTSIGRKPELYKQK-SVDSEGNKDD 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 151 QEKLGLTFLFSLEYNFERKAFVNNIKKARGHLPAMDEQSWTSDPYIKMTILPEKKHKVTRV 210
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 VKTCGLNFALQYDENELLVVKIILKALDPAKSTG-TSDPYVKIYLLPDRKKKQTRV 287
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 LRKTLDPADFETTFYGIPTQIQELALHFTILSDFRGRDDIIGEVLIPLSGIELSEK 270
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 HRKTLNPLFDELQF-PVYDQLSNRKLHFSYDFDRFRSHDMIGEVLID----NLFVS 342
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 MIMREIIRNVR-----KSSRGELLISLCYOSTTNTLTAVVLKARHLPKSDVSLSDPY 326
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 DLSREATVWKDIHCATTESMDLGEIMFSLCYLPTAGRMWLTWIKCRNLKAMDITGSSDPY 402
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 VKNLYHAKKRIKSKKTHVKKTPNAVFNELFVDIPCGLIEDISVEFLVLDSEGRSNE 386
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 403 VKVSLMCEGRLLKKRKTITTKNTLNPVNEALIFDIPPENVDQVSLCIAVMDYDRVGHNE 462
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 387 VIGQLVLGAAAGTGGEHMKICDYPKQIAKWHVL 422
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 463 VIGVCRIGLDAEGLGRDHWNEMLAYHRKPITHWHL 498
```

Search completed: February 20, 2004, 13:13:18
Job time : 18 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:10:35 ; Search time 39 Seconds
(without alignments)
2812.112 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREEFDEIPTVVGI.....KEICDYPRQIAKNHVLCDG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL 23:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organella:*
- 10: sp_phase:*
- 11: sp_plant:*
- 12: sp_rodent:*
- 13: sp_virus:*
- 14: sp_vertebrate:*
- 15: sp_unclassified:*
- 16: sp_rvirus:*
- 17: sp_bacteriap:*
- 18: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1999	90.8	425	11	Q8BGH3
2	1994	90.6	425	11	Q8BRL6
3	1160.5	52.7	430	11	Q925B6
4	1159	52.7	431	4	Q96SU2
5	1153	52.4	431	4	Q8IXU3
6	874	39.7	245	11	Q8QZS8
7	759	34.5	474	5	Q8SYD5
8	757	34.4	474	5	Q9UGP7
9	645.5	29.3	357	5	Q9GRB0
10	627.5	28.5	403	11	Q62747
11	627	28.5	424	5	Q25393
12	622.5	28.3	474	5	Q9VVG7
13	621.5	28.2	447	11	Q8CF96
14	621	28.2	403	5	Q07529
15	617.5	28.1	472	5	Q9VVG8
16	615.5	28.0	518	11	Q8CF95

17	615.5	28.0	520	11	Q99P37	Q99P37 rattus norv
18	615.5	28.0	523	11	Q99P36	Q99P36 rattus norv
19	615.5	28.0	567	11	Q99P35	Q99P35 rattus norv
20	615.5	28.0	611	11	Q99P34	Q99P34 rattus norv
21	615.5	28.0	643	11	Q99P33	Q99P33 rattus norv
22	615.5	28.0	687	11	Q99P38	Q99P38 rattus norv
23	613	27.9	429	5	Q9BMF3	Q9bmf3 manduca sex
24	606.5	27.6	419	4	Q8NBE5	Q8nbe5 homo sapien
25	603.5	27.4	422	11	Q8ROE1	Q8roel mus musculu
26	603	27.4	511	11	Q62746	Q62746 rattus norv
27	599.5	27.2	419	4	Q8N910	Q8n910 homo sapien
28	598	27.2	426	11	Q9QUK7	Q9quk7 mus musculu
29	598	27.2	511	11	Q9RON8	Q9ron8 mus musculu
30	597	27.1	438	11	Q8C8S6	Q8c8s6 mus musculu
31	589	26.8	523	11	Q925B8	Q925B8 rattus norv
32	588	26.7	395	5	Q9U8R6	Q9u8r6 dugesia jap
33	572	26.0	443	5	Q95QH7	Q95qh7 caenorhabdi
34	567.5	25.8	491	11	Q925C0	Q925C0 rattus norv
35	563.5	25.6	491	11	Q9RON9	Q9ron9 mus musculu
36	563.5	25.6	491	11	Q8C280	Q8c280 mus musculu
37	547	24.9	279	11	Q62748	Q62748 rattus norv
38	544.5	24.7	381	5	P91493	P91493 caenorhabdi
39	519.5	23.6	590	4	Q8N640	Q8n640 homo sapien
40	518.5	23.6	590	4	Q8N5Z1	Q8n5z1 homo sapien
41	516	23.4	588	11	Q925B7	Q925B7 rattus norv
42	481.5	21.9	470	11	Q920M7	Q920m7 mus musculu
43	474	21.5	474	11	Q62807	Q62807 rattus norv
44	464.5	21.1	474	4	Q9BSW7	Q9bsw7 homo sapien
45	463	21.0	474	4	Q9NZ18	Q9nzi8 homo sapien

ALIGNMENTS

RESULT 1

Q8BGH3 ID Q8BGH3 PRELIMINARY; PRT; 425 AA.
AC Q8BGH3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Synaptotagmin 4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Dorsal root ganglion, Medulla oblongata, and Pancreas;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK032106; BAC27705.1; -
DR EMBL; AK050515; BAC34301.1; -
DR EMBL; AK083960; BAC39080.1; -
SQ SEQUENCE 425 AA; 47659 MW; 9A01144898CDFCEB CRC64;

Query Match 90.8%; Score 1999; DB 11; Length 425;
Best Local Similarity 89.9%; Pred. No. 9.5e-139; Indels 0; Gaps 0;
Matches 382; Conservative 20; Mismatches 23;

QY 1 MAPITTSREEFDEIPTVVGIFSAFLVFTVSLFAWICCOCKSSKSNKTPPYKFVHLKGV 60

Db 1 MAPITTSREEFDEIPTVVGIFSAFLVFTVSLFAWICCOCKSSKSNKTPPYKFVHLKGV 60

QY 61 DYIPENLNKKFGADDKNEVKKNKPAVPKNSLHLDLEKRLDNGNFPKTNLKPSPSDLEN 120

Db 61 DYIPENLNKKFGADDKNEVKKNKPAVPKNSLHLDLEKRLDNGNFPKTNLKPSPSDLEN 120

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QY 121 ATPKFLBGEKESVSPESLKSSTSLTSEEKQKGLTFLFSLVNFERKAFVNNIKEARGL 180
Db 121 VTPKFLFETEKANSPELKSSTSLTSEEKQKGLTFLFSLVNFERKAFVNNIKEARGL 180
QY 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGYPTQIOELALHF 240
Db 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGYPTQIOELALHF 240
QY 241 TILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMREIIKENVKSSGRGELLISLCYQST 300
Db 241 TVLSFDRFSDDDIIGEVLIPLSGIELSDGKMLMREIIKENVKSSGRGELLISLCYQST 300
QY 301 TMTLVVVLKARHLPKSDVSGSLSDPYVKNLYHAKKRISKKKTHVKKCTPNAVFNELFVF 360
Db 301 TMTLVVVLKARHLPKSDVSGSLSDPYVKNLYHAKKRISKKKTHVKKCTPNAVFNELFVF 360
QY 361 DIPCEGLIEDISVEFLVLDSEGRSNEVIGOLVGAAGTGGHWEKICDYPFRQIAKWH 420
Db 361 DIPCESLEIISVEFLVLDSEGRSNEVIGRLVIGATAEGSGGHHWEKICDYPFRQIAKWH 420
QY 421 VLCDG 425
Db 421 MLCDDG 425

RESULT 2
Q8BRL6 PRELIMINARY; PRT; 425 AA.
AC Q8BRL6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Synaptotagmin 4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK043985; BAC31726.1;
SQ SEQUENCE 425 AA; 47658 MW; 60011E4F23A7F6EC CRC64;

Query Match 90.6%; Score 1994; DB 11; Length 425;
Best Local Similarity 89.6%; Pred. No. 2.2e-138;
Matches 381; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LPFWICCCQKSSKSNKTPPYKFFVHLKGV 60
Db 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LPFWICCCQKSSKSNKTPPYKFFVHLKGV 60
QY 61 DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDNGNPPKTNLKGSPSDLEN 120
Db 61 DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDNGNPPKTNLKGSPSDLEN 120
QY 121 ATPKFLBGEKESVSPESLKSSTSLTSEEKQKGLTFLFSLVNFERKAFVNNIKEARGL 180
Db 121 VTPKFLFETEKANSPELKSSTSLTSEEKQKGLTFLFSLVNFERKAFVNNIKEARGL 180
QY 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGYPTQIOELALHF 240
Db 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGYPTQIOELALHF 240
QY 241 TILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMREIIKENVKSSGRGELLISLCYQST 300
Db 241 TVLSFDRFSDDDIIGEVLIPLSGIELSDGKMLMREIIKENVKSSGRGELLISLCYQST 300

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QY 301 TMTLVVVLKARHLPKSDVSGSLSDPYVKNLYHAKKRISKKKTHVKKCTPNAVFNELFVF 360
Db 301 TMTLVVVLKARHLPKSDVSGSLSDPYVKNLYHAKKRISKKKTHVKKCTPNAVFNELFVF 360
QY 361 DIPCEGLIEDISVEFLVLDSEGRSNEVIGOLVGAAGTGGHWEKICDYPFRQIAKWH 420
Db 361 DIPCESLEIISVEFLVLDSEGRSNEVIGRLVIGATAEGSGGHHWEKICDYPFRQIAKWH 420
QY 421 VLCDG 425
Db 421 MLCDDG 425

RESULT 3
Q925B6 PRELIMINARY; PRT; 430 AA.
AC Q925B6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Synaptotagmin 11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306341; PubMed=9162066;
RA von Poser C., Ichtchenko K., Shao X., Rizo J., Sudhof T.C.;
RT "The evolutionary pressure to inactivate. A subclass of synaptotagmins
RT with an amino acid substitution that abolishes Ca2+ binding.";
RL J. Biol. Chem. 272:14314-14319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Shin O.-H., von Poser C., Ichtchenko K., Shao X., Rizo J.,
RA Sudhof T.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; AF375465; AAK56960.1;
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR Pfam; PF00168; C2; 2.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00004; C2 DOMAIN 2; 2.
SQ SEQUENCE 430 AA; 48267 MW; FEB06702BAC2AFB CRC64;

Query Match 52.7%; Score 1160.5; DB 11; Length 430;
Best Local Similarity 51.7%; Pred. No. 3.7e-77;
Matches 229; Conservative 77; Mismatches 104; Indels 33; Gaps 7;

QY 1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LPFWICCCQKSSKSNKTPPYKFFVHLK 58
Db 1 MAEITNTRPSFDVSPFAAGLIGASVLVVCVSVTFVFWTCCHQOAEKKHKTPPYKFIHMLK 60
QY 59 GVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEK-----RDNGNPP----- 106
Db 61 GISIYPTLNNKKKILIKVRDDKSHRESGNLLVNAESGLLSHDDPRGSPASCIQ 120
QY 107 ---KTNLKPSPSDLENATPKLFLGEEKESVSPESLKSSTSLTSEEKQKGLTFLFSLFLEY 163
Db 121 LPKRDYGEELRSPMTSLTP-----GSKPTSP-----SSPEEDVNLGSLTFSVDY 166
QY 164 NFERKAFVNNIKEARGLPAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFT 223
Db 167 NFEKALVVTIQEAHGLPVMGQGTQGGSDPYIKMTILPKRHEVTRVLRKTLDPVEDETFT 226
QY 224 TFGYPTQIOELALHFILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMREIIKENVK 283
Db 227 TFGYPTQIOELALHFILSFDRFSDDDIIGEVLIPLSGIELSEGKMLMREIIKENVK 286
QY 284 KSSGRGELLISLCYQSTNTLVVVLKARHLPKSDVSGSLSDPYVKNLYHAKKRISKKK 342
Db 287 KCTISRGELQVSYSQPVQAQMTVVVVLKARHLPKSDVSGSLSDPYVKNLYHAKKRISKKK 346

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343 THVKCTNAVFNELFVFDIPCEGLIEDISVEEFLVDLSDRGSRNEVGQVLGAAGGT-G 401
347 THVRKCTLNPFNFESFIYDIPDLDPDISIEFLVIDFRDTTKEVVGRLLGASHVTSSG 406
402 GEHWKEICDYPRROAKWHVLCD 424
    |||:||:|||||||:
407 AEHWRVESCPKPVAKWHSJSE 429
    |||:||:|||||||:

RESULT 4
ID Q96SU2 PRELMINARY; PRT; 431 AA.
DC AT Q96SU2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBRel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBRel. 23, Last annotation update)
DE Hypothetical protein FLJ14634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otseuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi R.T., Kakuy Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Iishi S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuo Y.,
RA Nimomyia K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC -! SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL: AK027540; BAB55186.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002149; LRI.
DR InterPro; IPR001565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00399; SYNAPTOTAGMN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PSF0004; C2_DOMAIN_2; 2.
DR Hypothetical protein.
SQ SEQUENCE 431 AA; 48250 MW; 25E0E26FCF8937AF CRC64;
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[illegible]

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Db      303 TVLDYRMGNKNDVIGRLILG--CNGTGAEHLHSDMLSPRRPIAQWHTL 350
RESULT 10
Q62747
ID      Q62747      PRELIMINARY;      PRT;      403 AA.
AC      Q62747;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Synaptotagmin VII (Synaptotagmin VIIIS).
GN      SYTVII.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RS      "Ca(2+)-dependent and -independent activities of neural and non-neural
RT      synaptotagmins."
RL      Nature 375:594-599 (1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Intestine;
RX      MEDLINE=95312080; PubMed=7791877;
RA      Li C., Ullrich B., Zhang J.Z., Anderson R.G., Brose N., Sudhof T.C.;
RA      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR      EMBL; U20106; AAA8725.1; -.
DR      EMBL; AF336854; AK01449.1; -.
DR      HSSP; P21707; IRSY.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR002149; LRI.
DR      InterPro; IPR001565; Synaptotagmin.
DR      Pfam; PF00168; C2; 2.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 2.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
SQ      SEQUENCE 403 AA; 45482 MW; 3153FD7FC1DBEEFB CRC64;

Query Match      28.5%; Score 627.5; DB 11; Length 403;
Best Local Similarity 36.2%; Pred. No. 4,7e-38;
Matches 153; Conservative 72; Mismatches 127; Indels 71; Gaps 11;

QY      27 VFTVSI-----FAMIC--CORKSSKNKTPPYKVFVHLKGVDIYPENLNSKKFGADD-- 77
Db      23 IITVSLVTVILCGLCHWCQKLGKRYK-----NSLETVGTDSG 62
QY      78 -----KNEVK-----NKPVPKNSLHLDLSEKRLDNGNFPKTNLKGPSDLENATPK 124
Db      63 RGRGKKAIKLPAGGKAVNTAPVPGQTPHDESDDR-----TEPRS-----SVSDLVN--- 109
QY      125 LFLEGEKSVSPESLKSSTSLTSEE-----KQKLGTLTFLPSLVNPKAFVNNIKARG 179
Db      110 -----SLTSEMMLSPGSEDEAHEGSRNLRGIRQFSVGNFQESTLTVKVMKAQE 161
QY      180 LPAMDQSMSTDPYIKMTILPKKHVKVTRVLRKTLDPADFETFTFYGIPYTOQLALH 239
Db      162 LPKAD-FSGTSDPFVKIYLLPKKHLETKVKRKNLNPWNHETFLFEGFPYKVVQILY 220
QY      240 FTILSFDRPSDDITGEVLIPISGIELSEKGMMLNREIIRNVRKSSGRGELLISLCYQS 299
Db      221 LQVLDYDRFSRNDPIGEVSIPLNKVLTQ--MQTFWKDLKPCSDGSGSRGELLISLCYNP 278
QY      300 TTNVTVVVLKARHPKSDVSGLSDPYKVNLYHAKRISKKTHVKCTPNVFNELFV 359
Db      279 SANSIIVNIIKARNLKAMDIGTSDPYKVMWLYKDKRVEKKTVTKRNLPNIFESFA 338
QY      360 FDIPEGLEDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGEHWKEICDYPRIQIAKW 419

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Db      339 FDIPEKLRRTTIITVMDKDKLSRNDVIGKIYLSWKSQGEVKGHWKMTARPPQVAQW 398
QY      420 HVL 422
Db      399 HQL 401
RESULT 11
Q25393
ID      Q25393      PRELIMINARY;      PRT;      424 AA.
AC      Q25393;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Synaptotagmin.
OS      Loligo pealeii (Longfin squid).
OC      Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC      Decapodiformes; Loliginidae; Loligo.
OX      NCBI_TaxID=6621;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Optic lobe;
RX      MEDLINE=9606684; PubMed=7479868;
RA      Mikoshiba K., Fukuda M., Moreira J.E., Lewis F.M.T., Sugimori M.,
RA      Niinobe M., Ilinas R.;
RT      "Role of the C2A domain of synaptotagmin in transmitter release as
RT      determined by specific antibody injection into the squid giant synapse
RT      preterminal."
RL      Proc. Natl. Acad. Sci. U.S.A. 92:10703-10707 (1995).
CC      -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR      EMBL; D63797; BAA09866.1; -.
DR      HSSP; P21707; IRSY.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR002149; LRI.
DR      InterPro; IPR001565; Synaptotagmin.
DR      Pfam; PF00168; C2; 2.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 2.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
SQ      SEQUENCE 424 AA; 47656 MW; P9733D3B10CFF3C0 CRC64;

Query Match      28.5%; Score 627; DB 5; Length 424;
Best Local Similarity 34.6%; Pred. No. 5.5e-38;
Matches 144; Conservative 75; Mismatches 137; Indels 60; Gaps 8;

QY      10 EFDEIPTVVVGIFSAFGLVFTVSLFAMTCCORKSSKNKTPPYKVFVHLKGVDIYPENLNS 69
Db      59 ELEKLPIMAILITCAGVLLFLVCGTYCCCKRRCRRGK----- 96
QY      70 KKKFGADDANEKVNKPAVPKNSLHLDLEKEDLNGNFPKTNLKGPSDLENATPKLFLEG 129
Db      97 -----KDGKKGLKGA-----VDLKGVLGNSIKKQVP-----DLEEL----- 130
QY      130 EKESVSPESLKSSTSLTSEEKQKLGTLTFLPSLVNPKAFVNNIKARGLPAMDQSM 189
Db      131 -----PMNMEDNEAESTKSEVKLGKLYSMDYDFQKGLTVNVIQAADLPQMD-MSGT 183
QY      190 SDPYIKMTILPKKHVKVTRVLRKTLDPADFETFTFYGIPYTOQLALHFTILSFDRFS 249
Db      184 SDPYKVVVLMPPDKKFKETKHVKRKNLNPVNESFTFNKNVYADITGKTLVFAIYDFDRFS 243
QY      250 RDDITGEVLIPISGIELSEKGMMLN-REIK--RNVRKSSGRGELLISLCYSTNTILTY 306
Db      244 KHDQIGQVQVAMNSIDL--GSVMEERDLTSPNDAEKENKLGDI CFSLRVPTAGKITV 301
QY      307 VVLKARHPKSDVSGLSDPYKVNLYHAKRISKKTHVKCTPNVFNELFVFDIPECG 366
Db      302 VILEAKNLKMDVGLSDPYKVISLMLNGKRINKKKTIVKKCTLNIPYNNESFAFEVPEQ 361
QY      367 LEDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGEHWKEICDYPRIQIAKWHL 422

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Db 362 IQKVSLLVTVVDYDRGTGCTSEPTGLGNSTGTGLRHWSMDLANRRPFAQWHTL 417

RESULT 12
Q9VOG7 PRELIMINARY; PRT; 474 AA.

ID Q9VOG7
DT CSOVG7;
DT DT 01-MAY-2000 (TEmBLrel. 13, Created)
DT 01-MAY-2000 (TEmBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TEmBLrel. 23, Last annotation update)
DE SVT protein.
GN SVT OR CG3139.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davidson P.L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Durbin K.J., Evangelian C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
DR EMBL; AF003582; AAF51205.1; -.
DR HSSP; P21707; 1BYN.
DR FlyBase; FBgn004242; cvt.
DR InterPro; IPRO00008; svt.
DR InterPro; IPRO02149; IRI.
DR InterPro; IPRO01565; Synaptotagmin.
DR Pfam; PF00168; C2; 2.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00339; SYNAPTOTAGMN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS00499; C2 DOMAIN 1; 2.
DR PROSITE; PS50004; C2 DOMAIN 2; 2.

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "the genome sequence of Drosophila melanogaster";
 Science 287:2185-2195(2000).
 [2]
 SEQUENCE FROM N.A.
 RA Celiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 Banzon J., An H., Baldwin D., Banson J., Beeson K.Y., Busam D.A.,
 Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
 Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 Phouanavong S., Pittman G.S., Furl V., Richards S., Scheeler F.,
 Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of Drosophila melanogaster genome";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 Tupy J.L., Bergman C., Berman B., Carlson J.W., Celiniker S.E.,
 Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of Drosophila melanogaster genome";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A.
 RA Adams M.D., Celiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 RA FlyBase;
 Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
 EMBL; AE003582; AAF51206.2; -.
 FlyBase; FBgn0004242; syt.
 InterPro; IPR000008; C2.
 InterPro; IPR002149; LRI.
 InterPro; IPR001565; Synaptotagmin.
 Pfam; PF00168; C2; 2.
 PRINTS; PR00360; C2DOMAIN.
 PRINTS; PR00399; SYNAPTOTAGMN.
 SMART; SM00239; C2; 2.
 PROSITE; PS00499; C2 DOMAIN 1; 2.
 PROSITE; PS00004; C2 DOMAIN 2; 2.
 Q SEQUENCE 472 AA; 53032 MW; 40BB77BB9D468FCA CRC64;

Query Match 28.1%; Score 617.5; DB 5; Length 472;
 Best Local Similarity 35.6%; Pred. No. 3.1e-37;
 Matches 155; Conservative 65; Mismatches 140; Indels 75; Gaps 12;
 Y 3 PTTTSREFFDEIPTVV-----GIFSAGLVFTVSLFAWICQKSSKSNKTPPYK 52
 b 88 PVTKKHVHGSEVTEVIAERTGLPTWGVVAIIILVFLVVGIIFFCVRRFLKRRYKDGK 147
 Y 53 FVHVLKGVDIYPENLNSKKFGADDKNEVKONKPAVPKNSLHLDLEKRLDNGNFPKTNLKP 112
 b 148 ---GKGGVD-----MKSQVLLG---SAYKRP-----DMEEL----- 173
 Y 113 GSPSDLENATPKLFEGEKESVPSLSKSTSLTSEEKQEKGLTFFSLEYNPERKAFVV 172

Db 174 -----TENAE-----EGDEE-----DKQSEQKLGRLNFKLVDYDFNSLAV 209
 QY 173 NIKKARGLPAMDQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPADFTTTFYIPYQ 232
 Db 210 TVIQAEELPALD-MGTSDPYKVVYLLPDKKKFETKVRKTLSPVFNETFTFKSLPYAD 268
 QY 233 IOELALHFTILSFRDRIIGEVLIPLSGIELSEKMLMNRILIKENVKSSR---G 289
 Db 269 AMNKTIVFAIFDFDRFSKHDQIGEVKVPCLTIDLAQ-TIEWRDLV--SVEGEGQEKLG 325
 QY 290 ELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCT 349
 Db 326 DICFSLRYVPTAGKLTVVILEAKNLKKMDVGGLSDPYVKTAIMQNGRLKKKTSIKKCT 385
 QY 350 ENAVNELFVFDIPCEGLEDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGSHWKEIC 409
 Db 386 LNPYNESFSPEVPFEQIKICLVVTVVDYDRIGTSEPIGRCTILGCMGTGTLRHHSDML 445
 QY 410 DYPRRQIAKWHVLC 424
 Db 446 ASPRPPIAQWHTLKD 460

Search completed: February 20, 2004, 13:14:11
 Job time : 41 secs

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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:11:10 / Search time 20 Seconds

(without alignments)

2043.584 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREDFEIPVVG.....KEICDPRQIAKHWLVCDG 425

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	91.1	425	2	159355
2	627.5	28.5	403	2	S58400
3	623.5	28.3	474	1	BMFR5Y
4	621	28.2	403	2	S33318
5	603.5	27.4	422	1	BMK72Y
6	603.5	27.4	422	2	A55417
7	603	27.4	511	2	S58399
8	594.5	27.0	537	2	JH0415
9	594	27.0	441	2	A40707
10	592	26.9	498	2	PC6300
11	581	26.4	422	1	BMH01Y
12	581	26.4	422	2	A45486
13	579.5	26.3	427	2	JH0413
14	577	26.2	421	2	S09595
15	575	26.1	424	2	I51210
16	574.5	26.1	439	2	JH0414
17	573.5	26.1	386	2	I59387
18	547	24.9	279	2	S58402
19	544.5	24.7	390	2	T28967
20	520	23.6	588	2	A53563
21	474	21.5	474	2	S68695
22	430.5	19.6	412	2	JC4921
23	415	18.9	257	2	T16355
24	408	18.5	704	2	A48097
25	394.5	17.9	681	2	JX0338
26	393.5	17.9	684	2	I58166
27	390.5	17.7	315	2	T32059
28	384.5	17.5	400	2	JC2473
29	377.5	17.2	504	2	T33485

ALIGNMENTS

RESULT 1

159355

synaptotagmin IV - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C/Accession: I59355; I58163

R/Vician, L.; Lim, I.K.; Ferguson, G.; Tocco, G.; Baudry, M.; Herschman, H.R.

Proc. Natl. Acad. Sci. U.S.A. 92, 2164-2168, 1995

A/Title: Synaptotagmin IV is an immediate early gene induced by depolarization in PC12

A/Reference number: I59355; MUID:95199312; PMID:7892240

A/Accession: I59355

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-425 <RES>

A/Cross-references: GB:I38247; NID:9598376; PIDN:AAA67327.1; PID:9598377

R/Ullrich, B.; Li, C.; Zhang, J.Z.; McMahon, H.; Anderson, R.G.; Geppert, M.; Sudhof, T

Neuron 13, 1281-1291, 1994

A/Title: Functional properties of multiple synaptotagmins in brain.

A/Reference number: I58163; MUID:95085772; PMID:7993622

A/Accession: I58163

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-425 <RES>

A/Cross-references: EMBL:U14398; NID:9550453; PIDN:AAA68519.1; PID:9550454

C/Superfamily: synaptotagmin; protein kinase C C2 region homology

F;147-262/Domain: protein kinase C C2 region homology <KC2A>

F;281-396/Domain: protein kinase C C2 region homology <KC2B>

Query Match

Best Local Similarity 91.1%; Score 2006; DB 2; Length 425;

Matches 382; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLFAWICQQRKSSKNKTPPYKVFVHLKGV 60

Db 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLFAWICQQRKSSKNKTPPYKVFVHLKGV 60

QY 61 DIYPENLNSKKKGADKNKVPKPAVKNLSHLDLKRDNGNPPKTNKPGSPSDLEN 120

Db 61 DIYPENLNSKKKGADKNKVPKPAVKNLSHLDLKRDNGNPPKTNKPGSPSDLEN 120

QY 121 ATPKFLFLEKEKESVSPESLKSSTLTSEEKQKLTGTFPSLEYNPERKAFVNNIKEARGL 180

Db 121 ATPKFLFLEKEKESVSPESLKSSTLTSEEKQKLTGTFPSLEYNPERKAFVNNIKEARGL 180

QY 181 PAMDEQSMTSDPYIKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGTPTQIQELALHF 240

Db 181 PAMDEQSMTSDPYIKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGTPTQIQELALHF 240

QY 241 TVLSDFRFRDVIIGVPLSGIELSGEGLMNRREIKRNVKSSGRGELLISLCYOST 300

Db 241 TVLSDFRFRDVIIGVPLSGIELSGEGLMNRREIKRNVKSSGRGELLISLCYOST 300

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:11:10 / Search time 20 Seconds

(without alignments)

2043.584 Million cell updates/sec

Title: US-09-680-121C-2

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Listing first 45 summaries

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PIR_76.*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	91.1	425	2	159355
2	627.5	28.5	403	2	S58400
3	623.5	28.3	474	1	BMFR5Y
4	621	28.2	403	2	S33318
5	603.5	27.4	422	1	BMK72Y
6	603.5	27.4	422	2	A55417
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11	581	26.4	422	1	BMH01Y
12	581	26.4	422	2	A45486
13	579.5	26.3	427	2	JH0413
14	577	26.2	421	2	S09595
15	575	26.1	424	2	I51210
16	574.5	26.1	439	2	JH0414
17	573.5	26.1	386	2	I59387
18	547	24.9	279	2	S58402
19	544.5	24.7	390	2	T28967
20	520	23.6	588	2	A53563
21	474	21.5	474	2	S68695
22	430.5	19.6	412	2	JC4921
23	415	18.9	257	2	T16355
24	408	18.5	704	2	A48097
25	394.5	17.9	681	2	JX0338
26	393.5	17.9	684	2	I58166
27	390.5	17.7	315	2	T32059
28	384.5	17.5	400	2	JC2473
29	377.5	17.2	504	2	T33485

QY 301 TMTLVVVLKARHLPKSDVSGISDPVVKVNLVYHAKRIISKKTHVKKCTPNVFNELFVF 360
 DB 301 TMTLVVVLKARHLPKSDVSGISDPVVKVNLVYHAKRIISKKTHVKKCTPNVFNELFVF 360
 QY 361 DIPCEGLEDSVEFLVLDSEGRNEVIGQLVGLAAAGTGGHWEKEICDYPFRQIAKWH 420
 DB 361 DIPCEGLEDSVEFLVLDSEGRNEVIGQLVGLAAAGTGGHWEKEICDYPFRQIAKWH 420
 QY 421 VLCDG 425
 DB 421 MLCDG 425

RESULT 2
 S58400
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 13-Aug-1999
 C:Accession: S58400
 R;Li, C.; Ullrich, B.; Zhang, J.Z.; Anderson, R.G.W.; Brose, N.; Suedhof, T.C.
 Nature 375, 594-599, 1995
 A;Title: Ca(2+)-dependent and -independent activities of neural and non-neural synaptotagmin
 A;Reference number: S58399; MUID:95312080; PMID:7791877
 A;Accession: S58400
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-403 <LIC>
 A;Cross-references: EMBL:U20106; NID:9643655; PIDN:AAA87725.1; PID:G643656
 C;Superfamily: synaptotagmin; protein kinase C C2 region homology
 F;129-243/Domain: protein kinase C C2 region homology <KC2A>
 F;260-375/Domain: protein kinase C C2 region homology <KC2>

Query Match 28.5%; Score 627.5; DB 2; Length 403;
 Best Local Similarity 36.2%; Pred. No. 3.8e-36;
 Matches 153; Conservative 72; Mismatches 127; Indels 71; Gaps 11;

QY 27 VFTVSL-----FAWIC--CORKSSKNTPPYKFVHLKGVLDIYPENLNSKKFGADD-- 77
 DB 23 IITVSLVTIVLCGLCHWCQKRLGRYK-----NSLETGVTGPDG 62
 QY 78 -----KNEVK-----NKPAVPKNSLSHLDEKRLDNGNFKTNLKPSPSPLENATPK 124
 DB 63 RGRGEKKAIKLPAGGKAVNTAPVPGTQPHDESRR-----TEPRS-----SVSLVN----- 109
 QY 125 LFLGEXESVSPESIKSSTLSER-----KQKGLTFLFSLEYNPERKAFVNIKEARG 179
 DB 110 -----SLTSEMMLSPGSEDEAHEGCSRENIGRIQSFYNFOESTLTIVKVMKAQE 161
 QY 180 LPAMDEQMSSTDPIKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGIPYTOIQELALH 239
 DB 162 LPAKD-FSGTSDPFVKIYLLPDKKHLETKVKRKNLNPWNTEFLFEGFPYKVVQRILY 220
 QY 240 FTILSPFRSDDDIIGEVLIPLSGIELSEGMMLMREIIRKRVNKSRSRGELLISLCYQS 299
 DB 221 LQVLVDYRFRSNDPIGEVSIPLNKVDLTQ--MOTFWKDLKPCSDGSGRSELLSLCYNP 278
 QY 300 TTNLTIVVVLKARHLPKSDVSGISDPVVKVNLVYHAKRIISKKTHVKKCTPNVFNELFV 359
 DB 279 SANSIIVNIIKARNLKAMDIGTSDPYKVMWLMYKDKRVEKKTKVTKRNLNLPFNESFA 338
 QY 360 FDPICEGLEDSVEFLVLDSEGRNEVIGQLVGLAAAGTGGHWEKEICDYPFRQIAKWH 419
 DB 339 FDIPTKURETIIITVMDKDLKSLRNDVIGKLYLSWKSQPGFGEVHKWDMIAFRPQPAQW 398
 QY 420 HVL 422
 DB 399 HQL 401

RESULT 3
 BMFFSY
 synaptotagmin - fruit fly (Drosophila melanogaster)
 N;Alternate names: p65

C;Species: Drosophila melanogaster
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
 C;Accession: B39052
 R;Perin, M.S.; Johnston, P.A.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
 J. Biol. Chem. 266, 615-622, 1991
 A;Title: Structural and functional conservation of synaptotagmin (p65) in Drosophila ar
 A;Reference number: A39052; MUID:91093190; PMID:1840599
 A;Accession: B39052
 A;Molecule type: mRNA
 A;Residues: 1-474 <PER>
 A;Cross-references: GB:M55048; GB:J05711; NID:9158526; PIDN:AAA28925.1; PID:9158527
 C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are t
 C;Genetics:
 A;Gene: FlyBase:syt
 A;Cross-references: FlyBase:FBgn0004242
 A;Map position: 23B
 C;Superfamily: synaptotagmin; protein kinase C C2 region homology
 C;Keywords: duplication; membrane trafficking; phospholipid binding; synaptic vesicle;
 F;1-107/Domain: intravesicular #status predicted <INT>
 F;108-134/Domain: transmembrane #status predicted <EXT>
 F;135-474/Domain: extravesicular #status predicted <EXT>
 F;186-434/Region: phospholipid binding #status experimental
 F;186-300/Domain: protein kinase C C2 region homology <KC2A>
 F;319-434/Domain: protein kinase C C2 region homology <KC2B>

Query Match 28.3%; Score 623.5; DB 1; Length 474;
 Best Local Similarity 34.9%; Pred. No. 9.2e-36;
 Matches 152; Conservative 66; Mismatches 144; Indels 73; Gaps 9;

QY 3 PITTSREDFRIPVTV-----GIFSAGLVFTVSLFAWICQKSKSNKNTPPYK 52
 DB 88 FVIRKIHVGEVTVTEIAERTGLPTWGVVAIILVFLVFGIIFFCVRRFLKKRRTK-- 144
 QY 53 FVHLKGVLDIYPENLNSKKKGADDKNEVKKPAVPKNSLSHLDEKRLDNGNFKTNLKP 112
 DB 145 -----DGRGKKG-----VDMKSVQLLGSAYPEKVKQP 170
 QY 113 GSPSDLENATPKLLEGEKESVSPESIKSSTLSITSEKQKGLTLPFSLEYNPERKAFV 172
 DB 171 DMEELTENAE-----EGDEE-----DKSQKQLRLNPKLEYDFNNSLAV 211
 QY 173 NIKEARGLPAMDQMSSTDPIKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGIPY 232
 DB 212 TVIQAELPALD-MGTSDDPYKVVLLPDKKKFKETKVRKTLSPVNETFTPKSLPYAD 270
 QY 233 IQELALHTILSPFRSDDDIIGEVLIPLSGIELSEGMMLMREIIRKRVNKSRSR--G 289
 DB 271 AMNKTLPFAIFDFRFSKHDQIGEVKVPCLCTIDLAQ-TIEWRDLV--SYEGEGGQEKLG 327
 QY 290 ELLISLCYQSTTNTLTVVVLKARHLPKSDVSGISDPVVKVNLVYHAKRIISKKTHVKKCT 349
 DB 328 DICSLRVPVPTAGKUTVVILEARNLKKMDVGLSDPYVKIATMONGRLKKKTKTSVKCT 387
 QY 350 PNAVNELFVDIPCEGLEDSVEFLVLDSEGRNEVIGQLVGLAAAGTGGHWEKEIC 409
 DB 388 LNPYNESFSEVPPEQMKICLVTVVDYDRIGTSEPIGRCILGCMGTGTELHWSMDL 447
 QY 410 DYPRRQIAKWHVLC 424
 DB 448 ASRRPIAQWHTLKD 462

RESULT 4
 S33318
 synaptotagmin - longfin squid
 C;Species: Loligo pealeii (longfin squid)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
 C;Accession: S33318
 R;Bommert, K.; Charlton, M.P.; DeBello, W.M.; Chin, G.J.; Betz, H.; Augustine, G.J.
 Nature 363, 163-165, 1993
 A;Title: Inhibition of neurotransmitter release by C2-domain peptides implicates synapt
 A;Reference number: S33318; MUID:93247639; PMID:8097867
 A;Accession: S33318

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <BOM>
A;Cross-references: EMBL:X72386; NID:g311734; PIDN:CAA51079.1; PID:g311735
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;121-235/Domain: protein kinase C C2 region homology <KC2A>
F;255-370/Domain: protein kinase C C2 region homology <KC2B>

Query Match 28.2%; Score 621; DB 2; Length 403;
Best Local Similarity 35.6%; Pred. No. 1.1e-35;
Matches 149; Conservative 71; Mismatches 131; Indels 68; Gaps 10;

Qy 10 EFDIEPTVVGIFSAFGLVFTVSLFAWICQ---RKSSKSNKTPPYKFVHVHLKGVDPEN 66
Db 40 ELEKLPITWAILICAGVLLFLVCGTYCCCKRICRRRGKDKGKGLGAVDLRGVQLL--- 96
Qy 67 INSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNPKTNLKPSPSDLENATPKLF 126
Db 97 -----GNSIKEXP-----DLEELPMN-----MEDNEDA----- 119
Qy 127 LEGKESVPSLSKSTSLTSEKOKLGTLPFSLFYNFERKAFVNNKEARGLPAMDEQ 186
Db 120 -----ESTKS-----EVKLGKLYQVMDYDFQKGLTNNVIQAADLPQMD-M 159
Qy 187 SMTSDPYIKMTILPKKHVKTRVLRKTLDPAPDETFTFYGIPYTOIQELALHFTLSFD 246
Db 160 SGTSDPYVYKVLMPDKKKFKETKVRKTLNPNVFNESFTFNVPYADITGKTLVFAIYDFD 219
Qy 247 RFSRDDIIGEVLIPLSGIETLSGKLMN-RELIK-RNVKSSGRGELLISLCYQSTTNT 303
Db 220 RFSKHDQIGQVQVAVNSIDL--GSVWEERDITSPDDAEKENKLGIDCFSLRYVPAGK 277
Qy 304 LTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTPNPAVFNELFVFDIP 363
Db 278 LTVVILEAKNLKMDVGLSDPYKVISLMLNGRIKKKTKTKTLNPNYNSFAFEPV 337
Qy 364 CEGLEDISVEFLVLDSEGRSNEVIGQLVGLAAAGTGGEHNKEICDYPRRQIAKHVHL 422
Db 338 FEQIQKSLYTVVVDYDRHTWSEPIGRTELGCSNLTGRLHNSDMLANPRPPIAQHWTL 396

RESULT 5
BMR2Y
synaptotagmin II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A39454
R;Geppert, M.; Archer III, B.T.; Suedhof, T.C.
J. Biol. Chem. 266, 13548-13552, 1991
A;Title: Synaptotagmin II. A novel differentially distributed form of synaptotagmin.
A;Reference number: A39454; MUID:91310620; PMID:1856191
A;Accession: A39454
A;Molecule type: mRNA
A;Residues: 1-422 <GEP>
A;Cross-references: GB:M64488; NID:g207144; PIDN:AAA63502.1; PID:g207145
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are the C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;1-60/Domain: duplication; glycoprotein; membrane trafficking; phospholipid binding; synap F;1-60/Domain: intravesicular #status predicted <INT>
F;61-87/Domain: transmembrane #status predicted <TM>
F;88-422/Domain: extravesicular #status predicted <EXT>
F;136-392/Region: phospholipid binding #status predicted
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>
F;32/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.4%; Score 603.5; DB 1; Length 422;
Best Local Similarity 35.6%; Pred. No. 1.9e-34;
Matches 151; Conservative 63; Mismatches 127; Indels 83; Gaps 12;

Qy 10 EFDIEP-----TVVGIFSAFGLVFTVSLFA---WICQKSSKSNKTPPYKFVHVHLKGVDI 62
Db 57 EINKIPLPPWALIAMAVVAGLLLLTCCFCICCKCKCKKKNKKEKG-----KGM-- 105

Qy 63 YPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNPKTNLKPSPSDLENAT 122
Db 106 -KNAMNMKMDKGGQDDDDA-----ETGLTEG----- 130
Qy 123 PKLFLLEGKESVPSLSKSTSLTSEKOKLGTLPFSLFYNFERKAFVNNKEARGLP 182
Db 131 -----EGEGE-----EKEPENLGKLOFSLDYDFOANQLTVGVLOAAELPA 171
Qy 183 MDEQSMTSDPYIKMTILPKKHVKTRVLRKTLDPAPDETFTFYGIPYTOIQELALHFTI 242
Db 172 LD-MGTSDDPYVYKVLFPDKKKYETKVRKTLNPNAFNETFTP-KVPYQELGGKTLVMAI 229
Qy 243 LSFDRFSDDDIIGEVLIPLSGIEL-----SEGKMLMNRRIKRNVRKSSGRGELLISLCYQ 298
Db 230 YDFDRFSKHDIIIGEVKVPMTVDLQPIEWRDLQGE--KEEPEK---LGDICTSLRYV 284
Qy 299 STTNLTITVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTPNPAVFNELF 358
Db 285 PTAGKLTVCILEAKNLKMDVGLSDPYKVIHLQMONGRLKCKKTKTKTKTLNPNYNSF 344
Qy 359 VFDIPCEGLEDISVEFLVLDSEGRSNEVIGQLVGLAAAGTGGEHNKEICDYPRRQIAK 418
Db 345 SPEIPFEQIQKVOVVTVLDYDKLGKNEALGKIFVGSNAITGTELRHNSDMLANPRPPIAQ 404
Qy 419 WHVL 422
Db 405 WHSL 408

RESULT 6
A55417
synaptotagmin II - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 07-Jun-1996
C;Accession: A55417; B39454
R;Fukuda, M.; Aruga, J.; Nimobe, M.; Aimoto, S.; Mikoshiba, K.
J. Biol. Chem. 269, 29206-29211, 1994
A;Title: Inositol-1,3,4,5-tetrakisphosphate binding to C2B domain of IP4BP/synaptotagmin.
A;Reference number: A55417; MUID:95050743; PMID:7961887
A;Accession: A55417
A;Molecule type: mRNA
A;Residues: 1-422 <FUK>
A;Cross-references: GB:D37792; GB:D37793
R;Geppert, M.; Archer III, B.T.; Suedhof, T.C.
J. Biol. Chem. 266, 13548-13552, 1991
A;Title: Synaptotagmin II. A novel differentially distributed form of synaptotagmin.
A;Reference number: A39454; MUID:91310620; PMID:1856191
A;Accession: B39454
A;Molecule type: DNA
A;Residues: 377-422 <GEP>
A;Cross-references: GB:M64488
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: membrane trafficking
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>

Query Match 27.4%; Score 603.5; DB 2; Length 422;
Best Local Similarity 35.6%; Pred. No. 1.9e-34;
Matches 151; Conservative 63; Mismatches 127; Indels 83; Gaps 12;

Qy 10 EFDIEP-----TVVGIFSAFGLVFTVSLFA---WICQKSSKSNKTPPYKFVHVHLKGVDI 62
Db 57 EINKIPLPPWALIAMAVVAGLLLLTCCFCICCKCKCKKKNKKEKG-----KGM-- 105
Qy 63 YPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNPKTNLKPSPSDLENAT 122
Db 106 -KNAMNMKMDKGGQDDDDA-----ETGLTEG----- 130
Qy 123 PKLFLLEGKESVPSLSKSTSLTSEKOKLGTLPFSLFYNFERKAFVNNKEARGLP 182
Db 131 -----EGEGE-----EKEPENLGKLOFSLDYDFOANQLTVGVLOAAELPA 171

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QY 183 MDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAFDETFTFYGIPTQIOELALHPTI 242
D 172 LD-MGTSDPYKVFLLPDKKKYETVHKXTLNPANETFTF-KVYQOELGGKTLVMAI 229
QY 243 LSFDRSRDDIIIGVILPISGIEL-----SFGKMLMREIIRKRVKSSGRGELATSLCYQ 298
D 230 YDFDRFSKHDIIIGEVKVPMTVDLQGPIDRDLQGE--KEEPEK---LGDICTSLAYV 284
QY 299 STINTLTIVVVKARHLPKSDVSGLSDDPYKVNLYHAKRKISKKTHVKCTPNAVNELF 358
D 285 PTAGKLTVCILEAKNKKMDVGLSDPYKVIHLMQNGKRLKKKTKTKTKTLNPFVNESF 344
QY 359 VFDIPCEGLEDIISVEFLVLDSSGRSNEVIGQLVGLGAAAGTGGEHKKEICDYPRRQIAK 418
D 345 SHEIPFQIQKVQVVTVLDYDKLGNKALGKIPVGSNATGTELRHSDMLANPRPRPQAQ 404
QY 419 WHVL 422
D 405 WHSL 408

RESULT 7
S58399
cellutagmin I svtVI - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S58399
Nature 375, 594-599, 1995
A:Title: Ca(2+)-dependent and -independent activities of neural and non-neural synaptotagmin
A:Reference number: S58399; MUID:95312080; PMID:7791877
A:Accession: S58399
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <LIC>
A:Cross-references: EMBL:D20105; NID:9643653; PIDN:AAA87724.1; PID:9643654
C:Superfamily: synaptotagmin; protein kinase C C2 region homology
F:224-337/Domain: protein kinase C C2 region homology <KC2A>
F:356-471/Domain: protein kinase C C2 region homology <KC2B>

Query Match 27.4%; Score 603; DB 2; Length 511;
Best Local Similarity 40.4%; Pred. No. 2.7e-34;
Matches 127; Conservative 64; Mismatches 103; Indels 20; Gaps 6;

QY 115 PSDLENATPKLLEGKESVSPESLKSSTLSSEEKQELGTLFSLSEYNPERKAFVNI 174
D 202 PFSIGRIKELY---KQKSDGDEAKS-----EAAKSCGKINFSURYDESETLIVRI 251
QY 175 KEARGLPAMDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAFDETFTFYGIPTQIQ 234
D 252 LKAFDLPKADFCG-SSDPYKVIKLLPDRCKLQTRVHKTLNPTFDENFHF-PVPYIELA 309
QY 235 ELALHFTILSFDRSRDDIIIGVILPISGIELSEGKMLMREIIRKRVKSSGRGELATSLCYQ 298
D 310 DRKLHLSVDFDRFSRHDHMTGEVILD---NLFEASDLRSSTSIWKDIQVATSSVDLGE 365
QY 291 LLISLCYQSTNTLTIVVVKARHLPKSDVSGLSDDPYKVNLYHAKRKISKKTHVKCTP 350
D 366 INFSLCYLPTAGRLTITIKATNLKAMDITGSDPYKVIKLLPDRCKLQTRVHKTLNPTFDENFHF-PVPYIELA 425
QY 351 NAVFNELVFDIPCEGLEDIISVEFLVLDSSGRSNEVIGQLVGLGAAAGTGGEHKKEICD 410
D 426 NPVYNEALIFDIPPENMDQVSLISVMDYDRVGHNEIIGVCRVGISAGLGRDHWNEMIA 485
QY 411 YPRRQIAKWHVLCD 424
D 486 YPRKPIAHWHCLAE 499

RESULT 8
JH0415
synaptotagmin o-p65-C - electric ray (Discopyge ommata)
N:Alternate names: synaptic vesicle protein o-p65-C

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C:Species: Discopyge ommata
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-Aug-1999
C:Accession: JH0415
R:Wendland, B.; Miller, K.G.; Schilling, J.; Scheller, R.H.
Neuron 6, 993-1007, 1991
A:Title: Differential expression of the p65 gene family.
A:Reference number: JH0413; MUID:91273991; PMID:2054189
A:Accession: JH0415
A:Molecule type: mRNA
A:Residues: 1-537 <WEN>
A:Cross-references: GB:M64277; NID:G213112; PIDN:AAA49229.1; PID:9213113
A:Experimental source: electric organ
C:Superfamily: synaptotagmin; protein kinase C C2 region homology
C:Keywords: glycoprotein; membrane protein; synaptic vesicle
F:53-78/Domain: hydrophobic <HYD>
F:230-343/Domain: protein kinase C C2 region homology <KC2A>
F:362-477/Domain: protein kinase C C2 region homology <KC2B>

Query Match 27.0%; Score 594.5; DB 2; Length 537;
Best Local Similarity 31.5%; Pred. No. 1.1e-33;
Matches 156; Conservative 88; Mismatches 140; Indels 111; Gaps 19;

QY 6 TSREEFDEIPTVVGIFSAF-GLVFT-VSLF-AWICC-----QRKSKSNKTPPY 51
D 46 TRHIETDISVSLLSVIITFCGIVLLGVSLFVSKLWIPMRDKGLNPQRDSQHH---PH 102
QY 52 KVVH-----VLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSHLHLDLEKRLN 102
D 103 QHLHHHSHFTDLTVERVDCGPE-----MPERS-YLDLE----- 135
QY 103 GNFPKTNLK-----PGSPDL-----EN-----A 121
D 136 -SYPESGIKLSQTSPIPIVDTSSGSKENNIPNAHSQQQVSAPPATRENLSLRPIPQQLS 194
QY 122 TPKLFLGEKE-----SVSPESLKSSTLSSEEKQEL--GTLFSLSEYNPERKAFV 171
D 195 SPEFGTQADEKVEQVTSIGQIKPELYKQRSIDTEAKKHQKVCGRINFLRYTYTTEQLV 254
QY 172 VNKEARGLPAMDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAFDETFTFYGIPT 231
D 255 VKILKALDLPKADANGF-SDPYKVIKLLPDRCKLQTRVHKTLNPTFDENFHF-PVPYIELA 312
QY 232 QIQELALHFTILSFDRSRDDIIIGVILPISGIELSEGKMLMREIIRKRVKSSGRGELATSLCYQ 298
D 313 ELQNRKHLSEVYDFDRFSRHDIIQGVVLDNLFESDFSEDTTIW-RDILEATSEKAD-LG 370
QY 290 ELLISLCYQSTNTLTIVVVKARHLPKSDVSGLSDDPYKVNLYHAKRKISKKTHVKCTP 349
D 371 EINFSLCYLPTAGRLTITIKATNLKAMDITGSDPYKVIKLLPDRCKLQTRVHKTLNPTFDENFHF-PVPYIELA 430
QY 350 PNAVFNELVFDIPCEGLEDIISVEFLVLDSSGRSNEVIGQLVGLGAAAGTGGEHKKEIC 409
D 431 LNPVYNEALVFDIPPENMDQVSLISVMDYDRVGHNEIIGVCRVGISAGLGRDHWNEMIA 490
QY 410 DYPRRQIAKWHVLCD 424
D 491 ANPRKPIAHWHCLAE 505

RESULT 9
A40707
synaptotagmin - Caenorhabditis elegans
N:Alternate names: ric-2
C:Species: Caenorhabditis elegans
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 24-Sep-1999
C:Accession: A40707; T16226
R:Nonet, M.L.; Grundahl, K.; Meyer, B.J.; Rand, J.B.
Cell 73, 1291-1305, 1993
A:Title: Synaptic function is impaired but not eliminated in Caenorhabditis elegans mut
A:Reference number: A40707; MUID:93313960; PMID:8391930
A:Accession: A40707
A>Status: preliminary
A:Molecule type: mRNA

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A;Residues: 1-441 <NON>
A;Cross-references: GB:L15302; NID:g289717; PIDN:AAA28145.1; PID:g289718
R;Du, Z.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F31E8.
A;Reference number: Z18481
A;Accession: T16226
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-441 <DUZ>
A;Cross-references: EMBL:U55856; NID:g1280154; PID:g1280158; PIDN:AAA98023.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone F31E8
C;Genetics:
A;Gene: snt-1
A;Map position: 2
A;Intons: 39/2; 72/1; 132/3; 289/3; 329/1; 373/3; 408/2
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: membrane trafficking; transmembrane protein
F;153-266/Domain: protein kinase C C2 region homology <KC2A>
F;286-401/Domain: protein kinase C C2 region homology <KC2B>
Query Match 27.0%; Score 594; DB 2; Length 441;
Best Local Similarity 40.2%; Pred. No. 9.3e-34;
Matches 148; Conservative 57; Mismatches 111; Indels 52; Gaps 14;
QY 70 KKFGGADKNEVKNKPAVPKNSLHLDLEKRDINGNFPK-----TNLKPGSPSDLENAT 122
DB 97 RKLFGKRRHGE-KNK-----KGGKGGFGGQDVVDGKNIQ-GMAQDLSELG 141
QY 123 PKLFLGEGESVPSDELKSTSLTSEKQE-KLGLTFLFSLEYNFPERKAFVNIKEARGLP 181
DB 142 DAM-EONEKEQ-----AEEKEVKGRIQYKLDYDFOGQLTVTVIAQEDLP 187
QY 182 AMDEQSMSTDPYIKMTILPEKKHKVKTSLVRLDPADETFYFGIPYQIQELAHHT 241
DB 188 GMD-MGSTDPYVKYLLLPKPKKVKVETVHRKTLNPNVFNETPIF-KVAFNEITAKTLVPA 245
QY 242 ILSDFRSDRDIIIEVLPIPSGLISEGKMLMNRIL-----KRVKSSGGELLISLC 296
DB 246 IYDFRFSKHDQIQVILPGKIDL--GAVIEWKDIAPPPDDKEAKS--LGDICFSLR 301
QY 297 YQSTNTNTLVVVKARHLPKSDVSGLSDPYVKNLYHAKRISKKKTKHVKKTPNAVNE 356
DB 302 YVPTAGKLTVILEAKNKKMDVGLSDPYVKVILMQGKRLKKKTSIKKTLNPNYNE 361
QY 357 LFVFDIPCEGLEDSVLELVLDSEGRSNEVIGQLVGAABGTGGE--HWKEICDYPRR 414
DB 362 SFSEFVPEFIQVSLMITVMDYDKLSNDAIGRCLIG--CNGTGAEILRHWMMLASPRR 419
QY 415 QIAKWHVL 422
DB 420 PIAQWHTL 427
RESULT 10
PC6300
synaptotagmin X - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Accession: PC6300
R;Babity, J.M.; Armstrong, J.N.; Plumier, J.C.L.; Currie, R.W.; Robertson, H.A.
Proc. Natl. Acad. Sci. U.S.A. 94, 2638-2641, 1997
A;Title: A novel seizure-induced synaptotagmin gene identified by differential display.
A;Reference number: PC6300; MUID:97226006; PMID:9122248
A;Accession: PC6300
A;Molecule type: mRNA
A;Residues: 1-498 <SAB>
A;Cross-references: GB:U85513; NID:g1932800; PIDN:AA851686.1; PID:g1932801
C;Comment: This protein responses to seizure activity.
C;Genetics:
A;Gene: svt X
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: transmembrane protein

F;56-77/Domain: transmembrane #status predicted <TMM>
F;74-224/Domain: cytoplasmic #status predicted <CTY>
F;224-338/Domain: protein kinase C C2 region homology <KC2>
F;357-472/Domain: protein kinase C C2 region homology <KC2B>
Query Match 26.9%; Score 592; DB 2; Length 498;
Best Local Similarity 34.6%; Pred. No. 1.5e-33;
Matches 158; Conservative 72; Mismatches 156; Indels 70; Gaps 16;
QY 20 IFSAFGL-VFTVSLFA-WTCQCKSSKSNKTPPYKPVHLKGVVDIYPENLNS--KKKFGA 75
DB 60 VVSPCGALLVVSLEFVFWKLC-----WPCWKSCLVAPNVSTLPSISSAPTEVPET 110
QY 76 DDKNEV-KNKPAVPKNSLHLDLEKRDINGNFP-----KTNLK-----PGSPS 116
DB 111 EEKKEVENEKPAK-ALEPAKISHTSPDIAEVQFALKHEHLKHARVQRTDPTSSS 169
QY 117 -----DLENATPKLFLGEEKS-----VSPESLKSSTSLTSE-----EK 150
DB 170 RHNSFRRLPRQNMVSVDFSMGTPEVLQGETRTSIGRIKPELYKQK-SVDSEGNRKDD 228
QY 151 QEKLGTLFFSLEYNFERKAFVNIKEARGLPAMDEQSMSTDPYIKMTILPEKKHKVKTUV 210
DB 229 VKTCGKLNFAIQDYENELLVVKIIKALDLPKADSTG-TSDPYVKIYLLPDRKKKQFQTV 287
QY 211 LRKTLDPADFDETFYGIPTQIQELAHHTILSDRESRDDIIGEVILPLSGLESEGK 270
DB 288 HRKTLNPLFDELQF-PVYDQLSNRKLHFSIYDFDRSRHDMIGEVLID----NLFEVS 342
QY 271 MLNREIIRKVR-----KSSGRGELLISLCYSTNTLTAVVLKARHLPKSDVSGLSDPY 326
DB 343 DLSREATWKDIHCATTESMDLGEIMFSLCYLPTAGRMILTIVIKCNLKMADITGSSDPY 402
QY 327 VKNLYHAKRISKKKTKHVKKTPNAVNELVFVDPICBEGLEDISVEFLVLDSEGRSNE 386
DB 403 VKVSLMCEGRLLKRRKTKTKNTLNPVYNEAIIFDIPPENVDQVSLCIAVMDYDRVGHNE 462
QY 387 VIGQLVGAABGTGGEHWKELCIDYPRQIAKWHVL 422
DB 463 VIGVCRGTGLDAEGLGRDHWNEMLAYHRKEPITHWHEL 498
RESULT 11
BMHUY
synaptotagmin I - human
N;Alternate names: p65
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A39052
R;Perin, M.S.; Johnston, P.A.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 266, 615-622, 1991
A;Title: Structural and functional conservation of synaptotagmin (p65) in Drosophila and
A;Reference number: A39052; MUID:91093190; PMID:1840599
A;Accession: A39052
A;Molecule type: mRNA
A;Residues: 1-422 <PER>
A;Cross-references: GB:M55047; GB:J05710; NID:g338657; PIDN:AAA60609.1; PID:g338658
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are ti
C;Genetics:
A;Gene: GDB:SYT1; SYT
A;Cross-references: GDB:125296; OMIM:185605
A;Map position: 12cen-12q21
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: dimer; duplication; glycoprotein; membrane trafficking; phospholipid binding
F;1-53/Domain: intravesicular #status predicted <INT>
F;81-422/Domain: transmembrane #status predicted <TMM>
F;136-382/Region: phospholipid binding #status experimental
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>
F;25/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 26.4%; Score 581; DB 1; Length 422;

Best Local Similarity 39.9%; Pred. No. 7e-33;
Matches 132; Conservative 65; Mismatches 114; Indels 20; Gaps 8;
QY 105 FPKTNLKGSPSDLENATPKLFLGEGKESVSPSLK---SSTSLT-SEEK-----QKLG 155
DB 85 FKKNNKKKGKGGKGNAINMKDKGLKTKMDQALQDADDAETGLTGDGEEKPEEKELG 144
QY 156 TLFFSLYENFERKAFVNNIKKARGLPAMDEQSMSTDPYIKMTILPEKKHKVKTIVLRKTL 215
DB 145 KLOYSLDYDFQNNQLLVGIQAAELPALD-MGGSDFYKVFLLPDKKKKFETKVRKTL 203
QY 216 DPAFDETFTFYGPYTOIQELALHFTILSFDRSRDDIIGEVLIPLSGIEL-----SEGKM 271
DB 204 NPVNEQFTF-KVPYSELGKTLVMAVYDFDRFSKHDIIIGEFKVPMTVDFGHVTEWRD 262
QY 272 LMNREIIKRNVRKSSRGRELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYKVN 331
DB 263 LOSAE--KEEQEK---LGDICFSLRYVPTAGKTUTVILEAKNLKMDVGGSLDPYKVIHL 317
QY 332 YHAKKRISKKTHVKCTPNVFNELFVFDIPCEGLEDISVEFLVLDSEGRSNEVIGQL 391
DB 318 MONGKRLKKKTKTKNTLNPYNESFSEVPPEQIQKVQVVTVLDYDKIGNDAIGKV 377
QY 392 VLGAAGTGGEGHWEICDYPRIQIAKHVL 422
DB 378 FVGYNSTGAELRHWSMDLANPRPIAQWHTL 408

RESULT 12

A45486

synaptotagmin I - bovine
N/Alternate names: 39K protein; synaptic vesicle protein p65
C/Species: Bos primigenius taurus (cattle)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C/Accession: A45486; S19272
R/Davilecov, B.; Sontag, J.M.; Hata, Y.; Petrenko, A.G.; Fykse, E.M.; Jahn, R.; Sudhof, T.
J. Biol. Chem. 268, 6816-6822, 1993
A/Title: Phosphorylation of synaptotagmin I by casein kinase II.
A/Reference number: A45486; MUID:93203288; PMID:8454654
A/Accession: A45486

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-422 <DAV>

A/Cross-references: GB:L05922; NID:G945210; PIDN:AAA87360.1; PID:G945211

A/Experimental source: brain

A/Note: sequence extracted from NCBI backbone (NCBI:128028, NCBI:P128029)

R/Tugal, H.B.; van Leeuwen, F.; Apps, D.K.; Haywood, J.; Phillips, J.H.

Biochem. J. 279, 699-703, 1991

A/Title: Glycosylation and transmembrane topography of bovine chromaffin granule p65.

A/Reference number: S19272; MUID:92061982; PMID:1719959

A/Accession: S19272

A/Molecule type: protein

A/Residues: 113-132 <TUG>

C/Superfamily: synaptotagmin; protein kinase C C2 region homology

F:136-249/Domain: protein kinase C C2 region homology <KC2A>

F:267-382/Domain: protein kinase C C2 region homology <KC2B>

Query Match

Best Local Similarity 26.4%; Score 581; DB 2; Length 422;

Matches 132; Conservative 65; Mismatches 114; Indels 20; Gaps 8;

QY 105 FPKTNLKGSPSDLENATPKLFLGEGKESVSPSLK---SSTSLT-SEEK-----QKLG 155
DB 85 FKKNNKKKGKGGKGNAINMKDKGLKTKMDQALQDADDAETGLTGDGEEKPEEKELG 144

QY 156 TLFFSLYENFERKAFVNNIKKARGLPAMDEQSMSTDPYIKMTILPEKKHKVKTIVLRKTL 215
DB 145 KLOYSLDYDFQNNQLLVGIQAAELPALD-MGGSDFYKVFLLPDKKKKFETKVRKTL 203

QY 216 DPAFDETFTFYGPYTOIQELALHFTILSFDRSRDDIIGEVLIPLSGIEL-----SEGKM 271
DB 204 NPVNEQFTF-KVPYSELGKTLVMAVYDFDRFSKHDIIIGEFKVPMTVDFGHVTEWRD 262

QY 272 LMNREIIKRNVRKSSRGRELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYKVN 331
DB 263 LOSAE--KEEQEK---LGDICFSLRYVPTAGKTUTVILEAKNLKMDVGGSLDPYKVIHL 317
QY 332 YHAKKRISKKTHVKCTPNVFNELFVFDIPCEGLEDISVEFLVLDSEGRSNEVIGQL 391
DB 318 MONGKRLKKKTKTKNTLNPYNESFSEVPPEQIQKVQVVTVLDYDKIGNDAIGKV 377
QY 392 VLGAAGTGGEGHWEICDYPRIQIAKHVL 422
DB 378 FVGYNSTGAELRHWSMDLANPRPIAQWHTL 408

RESULT 13

JH0413

synaptotagmin o-p65-A - electric ray (Discopyge ommata)

N/Alternate names: synaptic vesicle protein o-p65-A

C/Species: Discopyge ommata

C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-Aug-1999

C/Accession: JH0413

R/Wendland, B.; Miller, K.G.; Schilling, J.; Scheller, R.H.

Neuron 6, 993-1007, 1991

A/Title: Differential expression of the p65 gene family.

A/Reference number: JH0413; MUID:91273991; PMID:2054189

A/Accession: JH0413

A/Molecule type: mRNA

A/Residues: 1-427 <WEN>

A/Cross-references: GB:M64275; NID:G213108; PIDN:AAA49227.1; PID:G213109

A/Experimental source: electric organ

C/Superfamily: synaptotagmin; protein kinase C C2 region homology

C/Keywords: glycoprotein; membrane protein; membrane trafficking; synaptic vesicle

F:58-84/Domain: hydrophobic <HYD>

F:141-254/Domain: protein kinase C C2 region homology <KC2A>

F:272-387/Domain: protein kinase C C2 region homology <KC2B>

F:267/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 26.3%; Score 579.5; DB 2; Length 427;

Matches 128; Conservative 66; Mismatches 115; Indels 21; Gaps 7;

QY 107 KTNLKGSPSDLENA-----TPKLFLEGEKESVSPSLKSTSLTS-----EEKQEKLG 156
DB 91 KKNKKKGKGGKGNAMTKDKVEMGKSGEQALQDDEDAETGLTDTGKEKEDEKLGK 150

QY 157 LFFSLYENFERKAFVNNIKKARGLPAMDEQSMSTDPYIKMTILPEKKHKVKTIVLRKTL 216
DB 151 LQFSLDYDFQNNQLLVGIQAAELPALDVG--TSDFYKVFLLPDKKKKFETKVRKTL 209

QY 217 DPAFDETFTFYGPYTOIQELALHFTILSFDRSRDDIIGEVLIPLSGIEL-----SEGKM 272
DB 210 NPVNEQFTF-KVPYSELGKTLVMAVYDFDRFSKHDIIIGEFKVPMTVDFGHVTEWRD 268

QY 273 MNREIIKRNVRKSSRGRELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYKVN 332
DB 269 QGAE--KEEQEK---LGDICFSLRYVPTAGKTUTVILEAKNLKMDVGGSLDPYKVIHL 323

QY 333 HAKKRISKKTHVKCTPNVFNELFVFDIPCEGLEDISVEFLVLDSEGRSNEVIGQL 392
DB 324 QNGKRLKKKTKTKNTLNPYNESFSEVPPEQIQKVQVVTVLDYDKIGNDAIGKV 383

QY 393 LGAAAGTGGEGHWEICDYPRIQIAKHVL 422

DB 384 VGYNSTAAELRHWSMDLANPRPIAQWHTL 413

RESULT 14

S09595

synaptotagmin P65 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Aug-1997

C/Accession: S09595; S20211

R/Perin, M.S.; Fried, V.A.; Mignery, G.A.; Jahn, R.; Sudhof, T.C.

Nature 345, 260-263, 1990

A;Title: Phospholipid binding by a synaptic vesicle protein homologous to the regulatory
A;Reference number: S09595; MUID:90238548; PMID:2333096
A;Accession: S09595
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-421 <PER1>
A;Accession: S20211
A;Molecule type: protein
A;Residues: 145-168;201-212;214-216;237-244;333-354;357-366;376-388;392-398 <PER2>
A;Note: 99-Asp, 116-Glu, and 232-Glu were also found
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: calmodulin binding; glycoprotein; membrane trafficking; synaptic vesicle; tr
F;1-52/Domain: intravesicular #status predicted <INT>
F;53-79/Domain: transmembrane #status predicted <TM>
F;80-421/Domain: extravesicular #status predicted <EXT>
F;135-248/Domain: protein kinase C C2 region homology <KC2A>
F;266-381/Domain: protein kinase C C2 region homology <KC2B>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.2%; Score 577; DB 2; Length 421;
Best Local Similarity 39.9%; Pred. No. 1.3e-32;
Matches 132; Conservative 64; Mismatches 115; Indels 20; Gaps 8;

QY 105 PPKYNLPGSPDLENATPKLFLEGEKESVSPESLK---SSTSILT-SEEK-----QKLG 155
DB 84 PKNKKNKKGKGGKGNAINMKDVOLGKTWKQALXDDDAETGLTGEKEEPKEEKLK 143

QY 156 TLFFSLENFERKAVVNIKEARGLPAMDEQSMTPDYIKMTTLPEKKHKVKTFLVLRKTL 215
DB 144 KLOYSLDYFQNNQLVGLIQAAELPALD-MGTSDDPYKVFLLPEKKKKFETKVRHRTL 202

QY 216 DPAFDETFYGIPTQIQLALHFTILSFDRSRDIIIEVLPLSGIEL----SEKGM 271
DB 203 NPVNEQTF-KVPSELGGKTLVMAVYDFDRSKHDIIGEYKVMNTVDFGHVTEWRD 261

QY 272 LMNREIIKRNVRKSSGRGELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYKVNVL 331
DB 262 LQSAE--KEQEK---LGDICFSLRVPTAGKLTVVILEAKNLKMDVGLSDPYVKIHL 316

QY 332 YHAKKRISKTHVKCTPNVFNELFVFDIPEGLEDISVEFLVLDSEGRSNEVIGQL 391
DB 317 MQNGKRLKKTKTKNTINPYNESFSFEVPEQIQKVQVVVTVLDYDKIGNDAIDKV 376

QY 392 VLGAAGTGGGHHKEICDYPRIAKWHVL 422
DB 377 FVGNSTGAELRHWSMDLANPRPRPTAQWHTL 407

RESULT 15
I51210
synaptotagmin p65 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I51210
E;Lou, X.; Bixby, J.L.
Dev. Biol. 159, 327-337, 1993
A;Title: Coordinate and noncoordinate regulation of synaptic vesicle protein genes durin
A;Reference number: I51210; MUID:93374184; PMID:8365570
A;Accession: I51210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-424 <LOU>
A;Cross-references: GB:S64957; NID:g409527; PIDN:AAB28081.1; PID:g409528
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;138-251/Domain: protein kinase C C2 region homology <KC2>
F;269-384/Domain: protein kinase C C2 region homology <KC2B>

Query Match 26.1%; Score 575; DB 2; Length 424;
Best Local Similarity 37.0%; Pred. No. 1.8e-32;
Matches 141; Conservative 71; Mismatches 129; Indels 40; Gaps 11;

QY 68 NSKKKEGADDKNEVKNKPAVPKNSLHLD-----LEKRDINGNFPKTNLKPGS 114

DB 44 NLKKKF----NMELNKIPLPPWALIAIAIVAVLLILTCCFCCLKCKCL---FKKKNKKKKK 96

QY 115 PSDLENATPKLFLEGEKESVSPESLK---SSTSILT-SEEK-----EKLGTLPFSLEYNF 165
DB 97 EKGKGNAINMKDVOLGKTWKQALXDDDAETGLTGEKEEPKEEKEKLGKIQLSLDYDF 156

QY 166 ERKAFVNIKEARGLPAMDEQSMTPDYIKMTTLPEKKHKVKTFLVLRKTLDPADDETTF 225
DB 157 QNNQLLVGLIQAAELPALD-MGTSDDPYKVFLLPEKKKKYETKVRHRTLNPEVNEQTF 215

QY 226 YGIPYTOIQLALHFTILSFDRSRDIIIEVLPLSGIEL----SEKMLMNRRIIKRN 281
DB 216 -KVPSELGGKTLVMAVYDFDRSKHDIIGEYKVMNTVDFGHVTEWRDLSAE--KEE 272

QY 282 VRKSSGRGELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISK 341
DB 273 QEK---LGDICFSLRVPTAGKLTVVILEAKNLKMDVGLSDPYVKIHLMQNGKRLKK 329

QY 342 KTHVKKCTPNVFNELFVFDIPEGLEDISVEFLVLDSEGRSNEVIGQLVLGAAGTGG 401
DB 330 KTTIKKNTINPYNESFSFEVPEQIQKVQVVVTVLDYDKIGNDAIDKVFVGYNSTGAE 389

QY 402 GEHWKEICDYPRIAKWHVL 422
DB 390 LRHWSMDLANPRPRPTAQWHTL 410

Search completed: February 20, 2004, 13:14:44
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:12:55 ; Search time 40 Seconds
(without alignments)
2224.687 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPITTSREDFEIPVTGGI.....KEICDPRRQIAKMHVLDG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 20938283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2201	100.0	425	11	US-09-954-570-2
2	1162	52.8	431	12	US-10-311-626-9
3	614	27.9	195	12	US-09-764-875-772
4	609	27.7	523	12	US-10-231-913-12
5	603	27.4	188	9	US-09-764-870-368
6	603	27.4	188	12	US-09-764-875-1072
7	603	27.4	188	15	US-10-125-540-368
8	603	27.4	461	9	US-09-764-870-365
9	603	27.4	461	15	US-10-125-540-365
10	603	27.4	511	12	US-10-231-913-82
11	598	27.2	511	12	US-10-231-913-81
12	592	26.9	498	12	US-10-231-913-80
13	590	26.8	523	12	US-10-231-913-79
14	589	26.8	523	12	US-10-231-913-78
15	581	26.4	906	12	US-10-307-389-6
					Sequence 2, Appli
					Sequence 9, Appli
					Sequence 772, Appl
					Sequence 82, Appl
					Sequence 368, Appl
					Sequence 1072, Ap
					Sequence 368, App
					Sequence 365, App
					Sequence 365, App
					Sequence 82, Appl
					Sequence 81, Appl
					Sequence 80, Appl
					Sequence 79, Appl
					Sequence 78, Appl
					Sequence 6, Appli

16	518.5	23.6	590	12	US-10-311-626-8	Sequence 8, Appli
17	507.5	23.1	295	9	US-09-764-870-364	Sequence 364, App
18	507.5	23.1	295	15	US-10-125-540-364	Sequence 364, App
19	447	20.3	413	11	US-09-764-870-364	Sequence 24, Appl
20	418	19.0	412	12	US-09-764-875-683	Sequence 683, Appl
21	395.5	18.0	373	12	US-09-764-875-770	Sequence 770, App
22	395.5	18.0	375	12	US-09-764-875-898	Sequence 898, App
23	344	15.6	199	12	US-09-764-875-771	Sequence 771, App
24	330	15.0	234	12	US-09-764-875-767	Sequence 767, App
25	330	15.0	267	9	US-09-764-870-359	Sequence 359, App
26	330	15.0	267	15	US-10-125-540-359	Sequence 359, App
27	321.5	14.6	671	12	US-10-311-626-5	Sequence 5, Appli
28	320.5	14.6	671	12	US-10-108-260A-2460	Sequence 2460, Ap
29	319.5	14.5	219	10	US-09-925-300-1448	Sequence 1448, Ap
30	301.5	13.7	555	12	US-10-104-047-2530	Sequence 2530, Ap
31	296.5	13.5	208	9	US-09-764-870-497	Sequence 497, App
32	296.5	13.5	208	12	US-09-764-875-1071	Sequence 1071, Ap
33	296.5	13.5	208	15	US-10-125-540-497	Sequence 497, App
34	254.5	11.6	501	15	US-10-177-293-447	Sequence 447, App
35	253	11.5	407	9	US-09-764-870-375	Sequence 375, App
36	253	11.5	407	15	US-10-125-540-375	Sequence 375, App
37	250	11.4	862	12	US-10-339-782-492	Sequence 492, App
38	250	11.4	910	15	US-10-177-293-449	Sequence 449, App
39	245	11.1	376	15	US-10-177-293-451	Sequence 451, App
40	238.5	10.8	203	12	US-10-029-386-34078	Sequence 34078, A
41	235.5	10.7	336	12	US-10-168-659-22	Sequence 22, Appl
42	235.5	10.7	348	9	US-09-764-870-502	Sequence 502, App
43	235.5	10.7	348	12	US-09-764-875-1068	Sequence 1068, Ap
44	235.5	10.7	348	15	US-10-125-540-502	Sequence 502, App
45	235	10.7	234	9	US-09-764-870-367	Sequence 367, App

ALIGNMENTS

RESULT 1

US-09-954-570-2
; Sequence 2, Application US/09954570
; Publication No. US20030033614A1
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Method for Identifying Horizontally Modulated Genes
; FILE REFERENCE: 267/116
; CURRENT APPLICATION NUMBER: US/09/954,570
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-570-2

Query Match 100.0%; Score 2201; DB 11; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-195;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAPITTSREDFEIPVTGGI	100.0%;	Score 2201;	DB 11;	Length 425;
Db	1	MAPITTSREDFEIPVTGGI	100.0%;	Pred. No. 1.3e-195;	Mismatches 0;	Indels 0;
Qy	61	DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDNGNFPKTNLKPSPSLEN	120			
Db	61	DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDNGNFPKTNLKPSPSLEN	120			
Qy	121	ATPKLFLGCEKESVSPESLKSSTLSLTSSEKQKLGTLFFSLEYNFERKAFVYNKEARGL	180			
Db	121	ATPKLFLGCEKESVSPESLKSSTLSLTSSEKQKLGTLFFSLEYNFERKAFVYNKEARGL	180			
Qy	181	PAMDQSMSTSDYIKMTIIPKXHKVTRVLRKTLDPAFDETFTFYGIPYQIOELAHFF	240			
Db	181	PAMDQSMSTSDYIKMTIIPKXHKVTRVLRKTLDPAFDETFTFYGIPYQIOELAHFF	240			


```
; Sequence 1072, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1072
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-1072
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Query Match 27.4%; Score 603; DB 12; Length 188;
Best Local Similarity 58.4%; Pred. No. 9.5e-48;
Matches 108; Conservative 41; Mismatches 34; Indels 2; Gaps 2;
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QY 242 ILSPFRSDDDIIGEVLLPLSGLESEGKMLMREIIRKRVKSSGRGELLISLCYQSTT 301
Db 3 VLSPFRSDDDIIGEVLLPLSGLESEGKMLMREIIRKRVKSSGRGELLISLCYQSTT 62
QY 302 NLTIVVLKARHLPKSDVSGLS-DPVYKVNLYHAKKRISKKTTHVKKCTPNAVENELFVF 360
Db 63 QMTVVVLKARHLPKMDITGLSGNPYKVNLYHAKKRISKKTTHVKKCTPNAVENELFVF 122
QY 361 DIPCEGLDISVEFLVLDSEGRSNEVIGQLVLGA-AAEGTGGHEHKEICDYPRRQIAKW 419
Db 123 DIPTDLLPDISIEFLVIDFDRITKNEVVGRLILGAHVSATAGAEHWEVCESPRKPVAKW 182
QY 420 HVLCDD 424
Db 183 HSLSE 187
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RESULT 7
US-10-125-540-368
; Sequence 368, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 368
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-125-540-368
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Query Match 27.4%; Score 603; DB 15; Length 188;
Best Local Similarity 58.4%; Pred. No. 9.5e-48;
Matches 108; Conservative 41; Mismatches 34; Indels 2; Gaps 2;
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QY 242 ILSPFRSDDDIIGEVLLPLSGLESEGKMLMREIIRKRVKSSGRGELLISLCYQSTT 301
Db 3 VLSPFRSDDDIIGEVLLPLSGLESEGKMLMREIIRKRVKSSGRGELLISLCYQSTT 62
QY 302 NLTIVVLKARHLPKSDVSGLS-DPVYKVNLYHAKKRISKKTTHVKKCTPNAVENELFVF 360
Db 63 QMTVVVLKARHLPKMDITGLSGNPYKVNLYHAKKRISKKTTHVKKCTPNAVENELFVF 122
QY 361 DIPCEGLDISVEFLVLDSEGRSNEVIGQLVLGA-AAEGTGGHEHKEICDYPRRQIAKW 419
Db 123 DIPTDLLPDISIEFLVIDFDRITKNEVVGRLILGAHVSATAGAEHWEVCESPRKPVAKW 182
QY 420 HVLCDD 424
Db 183 HSLSE 187
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RESULT 8
US-09-764-870-365
; Sequence 365, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 365
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-365
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Query Match 27.4%; Score 603; DB 9; Length 461;
Best Local Similarity 40.8%; Pred. No. 3.7e-47;
Matches 128; Conservative 62; Mismatches 104; Indels 20; Gaps 6;
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QY 115 PSDLENATPKLFLGEGKSVSPESLSKTSLSYSEEKQELGTLFFSLFSLYENPERKAFVYNI 174
Db 152 PTSIGRIKPELY--KQKSVDSGEDAKS-----EATKSCGKINFSLRYDYETETLIVRI 201
QY 175 KEARGLPAMDQSMSTDPYIKMTILPEKHKHVKTRVLRLKTLDPADFDETFTFYGIPTQIQ 234
Db 202 LKAFDLPKADFCG-SSDPYVKIYLLPDRKCKLQTRVHRKTLNPTFDENFHF-PVPYEELA 259
QY 235 ELALHFTILSDFRSDDDIIGEVLLPLSGLESEGKMLMREIIRKRVKSSGRGELLISLCYQSTT 290
Db 260 DRKLHLSVDFDRFSRHDIMGEVLD---NLFEASDLRSRETSIWKQIQYATSESDVLDGE 315
QY 291 LLISLCYQSTTNTLTVVLKARHLPKSDVSGLSGLSDPYKVNLYHAKKRISKKTTHVKKCTP 350
Db 316 INFSLCYLFTAGRLTLTVIKCRNLKAMDITGSDPYKVNLYHAKKRISKKTTHVKKCTP 375
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QY 351 NAVNELVFDPICGLEDISVEFLVLDSEGRNEVIGQLVLGAAAGTGGHHWKEICD 410
Db 376 NPVYNEAIIIFDIPENMDQVSLISVMDYDRVGHNEIIGVCRVGTAEGLGRDHWNEMLA 435
QY 411 YPRQRIAKHWLVD 424
Db 436 YPRKPIAHWSLVE 449

RESULT 9

US-10-125-540-365
; Sequence 365, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PFI141
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 365
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-365

Query Match 27.4%; Score 603; DB 15; Length 461;
Best Local Similarity 40.8%; Pred. No. 3.7e-47;
Matches 128; Conservative 62; Mismatches 104; Indels 20; Gaps 6;

QY 115 PSDLENATPKLFLGEGESVSPESLKSSTSLTSEKQKGLTFLFSLEYNFERKAFVNI 174
Db 152 PISIGRIKPELY---KQKSVGDDEAKS-----EATKSCGKINFSLRYDYETETLIVRI 201
QY 175 KEARGLPAMDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAPDETFYGIPTQIQ 234
Db 202 LKAFDLPKFCG-SSDPYKVIYLLPDRCKLQTRVHRKTLNPTFDENPHF-PVPYEELA 259
QY 235 ELALHFTILSFDRSRDDIIGEVILPLSGIELSECKMLNREIIRKNVR---KSSGRGE 290
Db 260 DRXLHLSVDFDRFSRDMICEVILD---NLFEASDLSTRETSIWKDIQVATSESDVLDGE 315
QY 291 LLISLCYQSTNTITLVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTP 350
Db 316 IMFSLCYLPFAGRLTLTVIKCNLKMADITGSDPYKVIYLLPDRCKLQTRVHRKTLNPTFDENPHF-PVPYEELA 375
QY 351 NAVNELVFDPICGLEDISVEFLVLDSEGRNEVIGQLVLGAAAGTGGHHWKEICD 410
Db 376 NPVYNEAIIIFDIPENMDQVSLISVMDYDRVGHNEIIGVCRVGTAEGLGRDHWNEMLA 435
QY 411 YPRQRIAKHWLVD 424
Db 436 YPRKPIAHWSLVE 449

RESULT 10

US-10-231-913-82
; Sequence 82, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsbrook II, John P.

; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zehusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 82
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-231-913-82

Query Match 27.4%; Score 603; DB 12; Length 511;
Best Local Similarity 40.4%; Pred. No. 4.4e-47;
Matches 127; Conservative 64; Mismatches 103; Indels 20; Gaps 6;

QY 115 PSDLENATPKLFLGEGESVSPESLKSSTSLTSEKQKGLTFLFSLEYNFERKAFVNI 174
Db 202 PISIGRIKPELY---KQKSVGDDEAKS-----EATKSCGKINFSLRYDYETETLIVRI 251
QY 175 KEARGLPAMDEQSMSTDPYIKWTILPEKKHKVKTIVLRKTLDPAPDETFYGIPTQIQ 234
Db 252 LKAFDLPKFCG-SSDPYKVIYLLPDRCKLQTRVHRKTLNPTFDENPHF-PVPYEELA 309
QY 235 ELALHFTILSFDRSRDDIIGEVILPLSGIELSECKMLNREIIRKNVR---KSSGRGE 290
Db 310 DRXLHLSVDFDRFSRDMICEVILD---NLFEASDLSTRETSIWKDIQVATSESDVLDGE 365
QY 291 LLISLCYQSTNTITLVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKCTP 350
Db 366 IMFSLCYLPFAGRLTLTVIKCNLKMADITGSDPYKVIYLLPDRCKLQTRVHRKTLNPTFDENPHF-PVPYEELA 425
QY 351 NAVNELVFDPICGLEDISVEFLVLDSEGRNEVIGQLVLGAAAGTGGHHWKEICD 410
Db 426 NPVYNEAIIIFDIPENMDQVSLISVMDYDRVGHNEIIGVCRVGTAEGLGRDHWNEMLA 485
QY 411 YPRQRIAKHWLVD 424
Db 486 YPRKPIAHWSLVE 499

RESULT 11

US-10-231-913-81
; Sequence 81, Application US/10231913
; Publication No. US20040005576A1

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; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, David A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Li, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zehusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-231-913-81

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Query Match      27.2%; Score 598; DB 12; Length 511;
Best Local Similarity 40.4%; Pred. No. 1.3e-46;
Matches 127; Conservative 63; Mismatches 104; Indels 20; Gaps 6;

QY 115 PSDLENATPKLFLGEKEVSPELSKSTSLTSEKQKGLFLFSLEYNFERKAFVMI 174
Db 202 PISGIRKPELY---KQKSVDDDAK-----EAAKSCGKINFSLDYSESLVRI 251
QY 175 KEARGLPAMDFQSMSTDPIYKMTILPEKKGKVKTVLRKTLDPARDETTFYGIPTQIQ 234
Db 252 LKAPFLPAKQFCG-SSDPYVKIYLLPDRCKLQTRVHRKTLNPTFDENFHF-PVPYEELA 309
QY 235 ELALHFTILSDFRSRDILIGELVPLSGIELSEGMNLRILKENVR-----KSSGRGE 290
Db 310 DRKLHLSVDFDRSRHMGIEVLDD----NLFASDLSRETSIWKDIQIATSESVDLGE 365
QY 291 LLSLCYQSTTNTLTVVVYLKARHLKPSDVSLSDPYVKVNLVYHAKKRISKKTHVKCTP 350
Db 366 IMFSLCYLPTAGRLTLTVIKCNLKAMQITGSDPYVKVSLCDGRLAKKTKTKNTL 425
QY 351 NAVNELFVFDIPCEGLEDISVEFLVLDSEGRNEVIGQLVLGAAAGTGGEHWEICD 410

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Db 426 NPVYNEAIFDIPPENMDQVSLLSVMDYDRVGHNEIIGVCRVGINAEGLRDHWNEMLA 485
QY 411 YPRRQIAKWHVLC D 424
Db 486 YPRKPIAHWSLIVE 499

RESULT 12
US-10-231-913-80
; Sequence 80, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zehusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-231-913-80

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Query Match      26.9%; Score 592; DB 12; Length 498;
Best Local Similarity 34.6%; Pred. No. 4.4e-46;
Matches 158; Conservative 72; Mismatches 156; Indels 70; Gaps 16;

QY 20 IFSAFGL-VFTVSLFA-WICQQRSSKSKTKTPYKFKVHLKGVDIYPENLNS--KKKFGA 75
Db 60 VVSCGIALLVSVLFFVFKLC-----WPCWKSCLVAPNVSTLPQSISSAPTEVET 110
QY 76 DDKNEV-KNKPAPKPNLSLHLDLEKRLNGNFP---KTNLK-----FGSPS 116

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111 DB EKKKEVEENKPAK-AIEPAIKISHTSPDIPAEVQTALKKEHLKHARVQRTDPTSS 169
117 QY -----DLENATPKLFEGEKES-----VSPESLKSSTSLTSE-----EK 150
170 DB RHNSFRHLPRQMNVSDFSMGTEPVLRQGETRTSIGRIKPELYKQK-SVDSEGNRKDD 228
151 QY QKIGTLFFSLEYNEFKAFVNNIKARGLPAMDEQSMSTDPYIKMTILPEKKHKVTRV 210
229 DB VTCGKLNLFALQDYENELLVVKIIFKALDLPKADSTG-TSDPYVKIYLLPDRKKKFQTRV 287
211 QY LRKTLDPAPDETFYGIPTQIOELALHFTILSDFRSRDDIIGEVLIPLSGIELSEK 270
288 DB HRKTLNPLFDELQF-PVYDQLSNRKLHRSIYDFDRSRHDMIGEVLID-----NLFEVS 342
271 QY MLMNREIKRNV-----KSSRGELLISLCYQSTNTLTVVVLKARHLPKSDVSGLSDPY 326
343 DB LLSREATVWKDIHCATTESDMLGEIMFSLCYLPTAGRWTLTVKCRNLKAMDITGSSDPY 402
327 QY VKVNLHAKRISKKTHVKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSEGRSNE 386
403 DB KVSMLCEGRLLKRRKTTTKNTLNPVYNEAIIFDIPPENVDQVSLCIAVMDYDRVGNE 462
387 QY VIGQLVGLAAAGTGGHEHKEICDYPFRQIAKHVLD 422
463 DB VIGVCTGLDAEGLGRDHNMELAYHRKEPITHWHPL 498

RESULT 13

US-10-231-913-79

; Sequence 79, Application US/10231913

; Publication No. US20040005576A1

; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia S.

; APPLICANT: Li, Li

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Vernet, Corine A.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Edinger, Schlomit

; APPLICANT: Peyman, John A.

; APPLICANT: Stone, David J.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Boldog, Ference L.

; APPLICANT: Colman, Steven D.

; APPLICANT: Eisen, Andrew J.

; APPLICANT: Liu, Xiaohong

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-216

; CURRENT APPLICATION NUMBER: US/10/231,913

; CURRENT FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: 60/251,660

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: 60/255,029

; PRIOR FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: 60/260,326

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/263,800

; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/269,942

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/286,183

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: 60/313,627

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/318,712

; PRIOR FILING DATE: 2001-09-12

; PRIOR APPLICATION NUMBER: 60/318,712

; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-231-913-79

Query Match 26.8%; Score 590; DB 12; Length 523;
Best Local Similarity 33.7%; Pred. No. 7.3e-46;
Matches 154; Conservative 74; Mismatches 161; Indels 68; Gaps 14;

QY 20 IFSAFGL-VFTVSLFA-WICQORSSKNKTPPVYKVFVHLKGVDIYPENLNS--KKKFGA 75
DB 60 VVSFCGLALLVSLFVFWKLC-----WPCWKSLLVAPNLVSLPQSISSAPTEVFET 110
QY 76 DDKNEVKN-----KPAVPKNSLHDL-----EKRDINGNFPKTNLKPQSPS- 116
DB 111 EEKKEVEENKPAKPAKATEPAIKISHTSPDIPAEVQTALKKEHLKHARVQRTTEPTSSR 170
QY 117 -----DLENATPKLFEGEKES-----VSPESLKSSTSLTSE-----EKQ 151
DB 171 HNSFRHLPRQMNVSDFSVGTETPILQRTGRTSIGRIKPELYKQK-SVDSEGNRKDDV 229
QY 152 EKLGTLLFFSLEYNEFKAFVNNIKARGLPAMDEQSMSTDPYIKMTILPEKKHKVTRVL 211
DB 230 KTCGKLNLFALQDYENELLVVKIIFKALDLPKADSTG-TSDPYVKIYLLPDRKKKFQTRV 288
QY 212 RKTLDPAFDETFYGIPTQIOELALHFTILSDFRSRDDIIGEVLIPLSGIELSEKGM 271
DB 289 RKTNLPLFDELQF-PVYDQLSNRKLHRSIYDFDRSRHDMIGEVLID-----NLFEVS 343
QY 272 LMNREIKRNV-----KSSRGELLISLCYQSTNTLTVVVLKARHLPKSDVSGLSDPY 327
DB 344 LSREATVWKDIHCATTESIDLGEIMFSLCYLPTAGRWTLTVKCRNLKAMDITGSSDPY 403
QY 328 KVNLYHAKRISKKTHVKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSEGRSNEV 387
DB 404 KVSMLCEGRLLKRRKTTTKNTLNPVYNEAIIFDIPPENVDQVSLCIAVMDYDRVGNEV 463
QY 388 IGQLVGLAAAGTGGHEHKEICDYPFRQIAKHVLD 424
DB 464 IGVCTGLDAEGLGRDHNMELAYHRKEPITHWHPL 500

RESULT 14

US-10-231-913-78

; Sequence 78, Application US/10231913

; Publication No. US20040005576A1

; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia S.

; APPLICANT: Li, Li

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Vernet, Corine A.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Edinger, Schlomit

; APPLICANT: Peyman, John A.

; APPLICANT: Stone, David J.

; APPLICANT: Ellerman, Karen

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Boldog, Ference L.

; APPLICANT: Colman, Steven D.

; APPLICANT: Eisen, Andrew J.

; APPLICANT: Liu, Xiaohong

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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:11:55 ; Search time 21 Seconds
(without alignments)
856.291 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201
Sequence: 1 MAPTTGREPDEIPTVVGI.....KEICDPRQIAKWHVLCDS 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2201	100.0	425	3	US-09-036-315-2
2	2006	91.1	425	3	US-09-036-315-5
3	605	27.5	121	3	US-09-036-315-7
4	581	26.4	422	3	US-08-872-979-8
5	577	26.2	113	3	US-09-036-315-10
6	361.5	16.4	355	3	US-08-872-979-7
7	338.5	15.4	375	3	US-08-872-979-3
8	310	14.1	60	3	US-09-036-315-24
9	288	13.1	138	2	US-08-609-049A-17
10	288	13.1	138	3	US-09-170-996-17
11	271	12.3	120	3	US-09-036-315-9
12	244	11.1	115	3	US-09-036-315-8
13	226	10.3	46	3	US-09-036-315-25
14	182.5	8.3	140	2	US-08-609-049A-16
15	182.5	8.3	140	3	US-09-170-996-16
16	182	8.3	95	4	US-09-800-971-10
17	180	8.2	34	3	US-09-036-315-22
18	169	7.7	33	3	US-09-036-315-26
19	166	7.5	31	3	US-09-036-315-21
20	158	7.2	916	4	US-09-417-197-73
21	158	7.2	1658	4	US-08-609-049A-13
22	158	7.2	1658	3	US-09-170-996-13
23	158	7.2	1726	2	US-08-609-049A-30
24	158	7.2	1726	3	US-09-170-996-30
25	157.5	7.2	136	2	US-08-609-049A-18
26	157.5	7.2	136	3	US-09-170-996-18
27	155.5	7.1	117	3	US-09-036-315-6

28 152.5 6.9 1876 2 US-08-609-049A-12 Sequence 12, Appl
29 152.5 6.9 1876 3 US-09-170-996-12 Sequence 12, Appl
30 149.5 6.8 137 2 US-08-609-049A-14 Sequence 14, Appl
31 149.5 6.8 137 3 US-09-170-996-14 Sequence 14, Appl
32 144.5 6.6 1876 2 US-08-609-049A-28 Sequence 28, Appl
33 144.5 6.6 1876 3 US-09-170-996-28 Sequence 28, Appl
34 144 6.5 1686 4 US-09-355-160D-2 Sequence 2, Appl
35 141 6.4 671 6 5266464 Patent No. 5266464
36 136 6.2 804 3 US-08-909-954-2 Sequence 2, Appl
37 131.5 6.0 799 3 US-08-909-954-4 Sequence 4, Appl
38 129.5 5.9 137 2 US-08-609-049A-15 Sequence 15, Appl
39 129.5 5.9 137 3 US-09-170-996-15 Sequence 15, Appl
40 125 5.7 25 3 US-09-036-315-23 Sequence 23, Appl
41 117 5.3 40 4 US-09-023-905A-31 Sequence 31, Appl
42 117 5.3 927 3 US-08-895-601-6 Sequence 6, Appl
43 109 5.0 990 2 US-08-392-625-20 Sequence 20, Appl
44 109 5.0 990 2 US-08-466-961A-20 Sequence 20, Appl
45 102.5 4.7 990 2 US-08-645-193B-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-036-315-2
; Sequence 2, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-036-315-2

Query Match 100.0%; Score 2201; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 9.6e-217;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAPITTSREDFEIPVTVGIFSAFGLVFTVSLFAWICQKSSKSNKTPPYKVFVHLKGV 60
Db 1 MAPITTSREDFEIPVTVGIFSAFGLVFTVSLFAWICQKSSKSNKTPPYKVFVHLKGV 60
QY 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
Db 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
QY 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNFERKAFVNNIKEARGL 180
Db 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNFERKAFVNNIKEARGL 180
QY 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLDPAFDEFTTFYGIPTQIQELALHF 240
Db 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLDPAFDEFTTFYGIPTQIQELALHF 240
QY 241 TILSFDRFSRDDIIGEVLIPLSGIELSGKMLMNRRIKRNVRKSSGRGELLISLCYQST 300
Db 241 TILSFDRFSRDDIIGEVLIPLSGIELSGKMLMNRRIKRNVRKSSGRGELLISLCYQST 300
QY 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKCTPNVAFNELFVF 360
Db 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKCTPNVAFNELFVF 360
QY 361 DIPCEGLEDISVEFLVLDSEKSRNEVIGQLVGAAGTGGEHWKEICDYPRROIAKWH 420
Db 361 DIPCEGLEDISVEFLVLDSEKSRNEVIGQLVGAAGTGGEHWKEICDYPRROIAKWH 420
QY 421 VLCDG 425
Db 421 VLCDG 425
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RESULT 2

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US-09-036-315-5
; Sequence 5, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
```

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..425
; OTHER INFORMATION: /note= "rat synaptotagmin 4 (SYT4)"
US-09-036-315-5
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Query Match 91.1%; Score 2006; DB 3; Length 425;
Best Local Similarity 89.9%; Pred. No. 8,9e-197;
Matches 382; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAPITTSREDFEIPVTVGIFSAFGLVFTVSLFAWICQKSSKSNKTPPYKVFVHLKGV 60
Db 1 MAPITTSREDFEIPVTVGIFSAFGLVFTVSLFAWICQKSSKSNKTPPYKVFVHLKGV 60
QY 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
Db 61 DIYPENLNKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
QY 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNFERKAFVNNIKEARGL 180
Db 121 ATPKLFLEGEKESVSPSLKSTSLTSEKQKGLTLPFSLEYNFERKAFVNNIKEARGL 180
QY 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLDPAFDEFTTFYGIPTQIQELALHF 240
Db 181 PAMDEQSMTSDPYIKMTILPEKHVKTRVLRTKLDPAFDEFTTFYGIPTQIQELALHF 240
QY 241 TILSFDRFSRDDIIGEVLIPLSGIELSGKMLMNRRIKRNVRKSSGRGELLISLCYQST 300
Db 241 TILSFDRFSRDDIIGEVLIPLSGIELSGKMLMNRRIKRNVRKSSGRGELLISLCYQST 300
QY 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKCTPNVAFNELFVF 360
Db 301 TNLTVVVLKARHLPKSDVSLSDPYKVNLYHAKKRISKKTTHVKCTPNVAFNELFVF 360
QY 361 DIPCEGLEDISVEFLVLDSEKSRNEVIGQLVGAAGTGGEHWKEICDYPRROIAKWH 420
Db 361 DIPCEGLEDISVEFLVLDSEKSRNEVIGQLVGAAGTGGEHWKEICDYPRROIAKWH 420
QY 421 VLCDG 425
Db 421 VLCDG 425
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RESULT 3

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US-09-036-315-7
; Sequence 7, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,246
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..121
OTHER INFORMATION: /note= "Repro-PC-1.0 (PC-20) "B"
OTHER INFORMATION: internal repeat (amino acid
positions 276-397)"
US-09-036-315-7

Query Match 27.5%; Score 605; DB 3; Length 121;
Best Local Similarity 99.2%; Pred. No. 3.5e-54;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2Y 276 EIIKRNVRKSSGRGELLISLCYQSTTNLTIVVVKARHLPKSDVSGLSDPYVKVNLVYHAK 335
DB 1 EIIKRNVRKSSGRGELLISLCYQSTTNLTIVVVKARHLPKSDVSGLSDPYVKVNLVYHAK 60

2Y 336 KRISKKTHVKCTPNVAVNELFVDFDIPCEGLEDSISVEFLVLDSEGRSNEVIGQLVLGA 395
DB 61 KRISKKTHVKCTPNVAVNELFVDFDIPCEGLEDSISVEFLVLDSEGRSNEVIGQLVLGA 120

2Y 396 A 396
DB 121 A 121

RESULT 4
US-08-872-979-8
Sequence 8, Application US/08872979
Patent No. 6074844
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,979
FILING DATE: Herewith
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```
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0320 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 338658
US-08-872-979-8

Query Match 26.4%; Score 581; DB 3; Length 422;
Best Local Similarity 39.9%; Pred. No. 7.5e-51;
Matches 132; Conservative 65; Mismatches 114; Indels 20; Gaps 8;

QY 105 FPKTNLKPSPDLENATPKLFLEGEKESVSPESLK---SSTSILT-SSEK-----QEKLG 155
DB 85 FKKNNKKKGEKGGKNAINMKVDKGLTKMDQALKDDDAETGLTDGEEKKEPEKEKLG 144

QY 156 TLFFSLVYNERKAFVNVNIKEARGLPAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTL 215
DB 145 KQVSLDYDFQNNQLLVGIIQAELPALD-MGTSDDPYVKVFLPLDPKKKFKFKVIRKTL 203

QY 216 DPAPDETFTYIGIPYTOIQELALHFTILSFDRFSRDDIIGEVLLIPLSGIEL-----SEGKM 271
DB 204 NPVNEQFTF-KVPYSELGKTLVMAVYDFDRFSKHDIIIGEFKVPMTVDVFGHVTEWRD 262

QY 272 LMNREILKRNVRKSSGRGELLISLCYQSTTNLTIVVVKARHLPKSDVSGLSDPYVKVNL 331
DB 263 LQSAE--KEEQEK--LGDICFSLRYVPTAGKLTVVILEAKNLKMDVGLSDPYVKVNIHL 317

QY 332 YHAKRISKKTHVKCTPNVAVNELFVDFDIPCEGLEDSISVEFLVLDSEGRSNEVIGOL 391
DB 318 MONGKRLKKKTKTKNTLNPYNESFSEFVEFQIQVQVVVVVLDYDKIGKNDATGKV 377

QY 392 VLGAAGGTGGEHWKEICDYPRRQIAKWHVL 422
DB 378 FVGYNSTGAELRHWSMDLANPRRPIAQWHTL 408

RESULT 5
US-09-036-315-10
Sequence 10, Application US/09036315
Patent No. 6218523
GENERAL INFORMATION:
APPLICANT: French, Cynthia K.
APPLICANT: Schneider, Patrick A.
APPLICANT: Yamamoto, Karen K.
TITLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Stozella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "Repro-PC-1.0 (PC-20) "A"
; OTHER INFORMATION: internal repeat (amino acid
; OTHER INFORMATION: positions 150-263)"
; US-09-036-315-10

Query Match 26.2%; Score 577; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 KOEKLGTILFFSLEYNFERKAFVNNIKKARGLPAMDEQSMTPYIKMTILPEKKHKVKTR 209
Db 1 KOEKLGTILFFSLEYNFERKAFVNNIKKARGLPAMDEQSMTPYIKMTILPEKKHKVKTR 60

QY 210 VLKTLDPAPDETFTFYGIPYQIOELALHFTILSDFRSDRIIGEVLIPLS 262
Db 61 VLKTLDPAPDETFTFYGIPYQIOELALHFTILSDFRSDRIIGEVLIPLS 113

RESULT 6
US-08-872-979-7
; Sequence 7, Application US/08872979
; Patent No. 6074844
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,979
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0320 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 643658
; US-08-872-979-7

Query Match 16.4%; Score 361.5; DB 3; Length 355;
Best Local Similarity 30.2%; Pred. No. 1.7e-28;
Matches 94; Conservative 62; Mismatches 120; Indels 35; Gaps 6;

QY 130 EKESVSPESLKSSTSLTSEEK-----QEKLGTLFFSLEYNFERKAFVNNIKKAR 178
Db 39 DKETVGLGSARNSTTHLVQPDVDCLEPCSGGDQWGRLLLSLEYDFGSGQEIIVGLRQAG 98

QY 179 GLPAMDEQSMTPYIKMTILPEKKHKVKTRVLKTLDPAPDETFTFYGIPYQIOELAL 238
Db 99 NLKA---EGTADPYAVWSVSTQSGRRHETKVRHGTLSPMFEETCCFL-VPPAELPKATL 153

QY 239 HFTILSDFRSDRIIGEVLIPLSGLIELSEKMLNREIKR-----NVRKSSGRGEL 291
Db 154 KVLQWDFKRFSEHEPLGELQLPLGTVDL-----QHVLESWYQLGPPGTTEPEQMDEL 205

QY 292 LISLCYQSTTNLTIVVVLKARHLPKSDVSGLSDPYVKNLYHAKKRISKKKTHVKKCTPN 351
Db 206 CFSRLYVPSGSLTIVVLEARGLN-----PLAEAYVKIQLMLNQRKWKSKTSKKGTTT 261

QY 352 AVFNELFVDFIPCEGLEIDISVEFLVDSRGRNEVIGQLVGLAAAGTGGHEHWKEICDY 411
Db 262 PYFNEAFVLPVSQVQLQSDVLVLAHWARGQLRTEPVGKVLGSRASSQPLQHWADMLAH 321

QY 412 PRQIAKWHVL 422
Db 322 ARRPQAQWHL 332

RESULT 7
US-08-872-979-3
; Sequence 3, Application US/08872979
; Patent No. 6074844
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,979
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/872,979
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0320 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGN0T12
; CLONE: 1003941
;
; US-08-872-979-3

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Query Match 15.4%; Score 338.5; DB 3; Length 375;
Best Local Similarity 29.8%; Pred. No. 4.2e-26;
Matches 91; Conservative 61; Mismatches 118; Indels 35; Gaps 6;

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130 EKESVSPESLKSSTSL-----TSEKQKGLTGLFSLVYPERKAFVNIKEAR 178
69 DRESVGLSGARGTTHLVQPDVDGLESPFGDAQWGRQLQLSLEFDFGQIRVGLRQAA 128
179 GLPAMDEQSMTPYIKMTILPEKKHKVTKVLRKTLDPAPDENFTFYGIPYTOIQELAL 238
129 DL-----MPGGTVDPYARVSVSTQAGHRHETKVHRTGTCVPEDETCFHF-IPQAEIPGATL 183
239 HFTILSFDRSDIIGELVLIPIISGLISEGKMLMNRRIKK-----NVRKSSGRGEL 291
184 QVOLFNFKFSGHEPGLERLAGTVDL-----QHVLEHWILGPPATQPPQVQEL 235
292 LISLCYQSTNTLTIVVVLKARHLPKSDVSGLSDFYKVNLYHAKKRISKKTHVKKCTPN 351
236 CFSRLRVPSGRLTVVVLGARGLR-----PGLAEFYKVLQMLNQRKWKKRKTATKGTAA 291
352 AVFNELFVDIPCEGLDISVEFLVLDSEGRSNEVIGQLVLGAAAGTGGEHKWEICDY 411
292 PYFNEAFTLVPPFSQVQNVLDLVLAVWDRSLPLRTPVPVKVHLGARASQPLQHWADMLAH 351
412 PRQI 416
352 AAREV 356

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RESULT 8
; US-036-315-24
; Sequence 24, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-09-036-315-24

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Query Match 14.1%; Score 310; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 LPBKHKVTKVLRKTLDPAPDENFTFYGIPYTOIQELALHFTILSFDRSDIIGEVL 258
Db 1 LPBKHKVTKVLRKTLDPAPDENFTFYGIPYTOIQELALHFTILSFDRSDIIGEVL 60

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RESULT 9
; US-08-609-049A-17
; Sequence 17, Application US/08609049A
; Patent No. 5948664
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Moiz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,049A
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-049A-17
Query Match 13.1%; Score 288; DB 2; Length 138;
Best Local Similarity 46.8%; Pred. No. 1.3e-21;
Matches 59; Conservative 22; Mismatches 45; Indels 0; Gaps 0;

QY 289 GELLISLCYQSTNTNLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKC 348
Db 12 GDICTSLRYVPTAGKLTVCILLEAKNLKMDVGLSDPYVKIHLQMONGKRLKXKKTIVKXK 71

QY 349 TPNVAFNELFVFDIPCEGLDISEVFLVLDSESGSNEVIGQLVLAAGTGEHWKEI 408
Db 72 TLNPFNFESFSEIPFEIQKQVQVVTVLDYDKLGKNEAIGKIFVGSNATGTLRHWSDM 131

QY 409 CDYPRR 414
Db 132 LANPRR 137

RESULT 10
US-09-170-996-17
; Sequence 17, Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,996
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,049
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
US-09-170-996-17
Query Match 13.1%; Score 288; DB 3; Length 138;
Best Local Similarity 46.8%; Pred. No. 1.3e-21;
Matches 59; Conservative 22; Mismatches 45; Indels 0; Gaps 0;

QY 289 GELLISLCYQSTNTNLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKC 348
Db 12 GDICTSLRYVPTAGKLTVCILLEAKNLKMDVGLSDPYVKIHLQMONGKRLKXKKTIVKXK 71

QY 349 TPNVAFNELFVFDIPCEGLDISEVFLVLDSESGSNEVIGQLVLAAGTGEHWKEI 408
Db 72 TLNPFNFESFSEIPFEIQKQVQVVTVLDYDKLGKNEAIGKIFVGSNATGTLRHWSDM 131

QY 409 CDYPRR 414
Db 132 LANPRR 137

RESULT 11
US-09-036-315-9
; Sequence 9, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
; OTHER INFORMATION: /note= "synaptotagmin "A" internal
; OTHER INFORMATION: repeat (amino acid positions 134-254) "
US-09-036-315-9
Query Match 12.3%; Score 271; DB 3; Length 120;
Best Local Similarity 45.3%; Pred. No. 5.5e-20;
Matches 53; Conservative 29; Mismatches 33; Indels 2; Gaps 2;

QY 149 EQEKLGITLFFSLEYNFERKAFVNTKEARGLPAMDEQSWTSIDYIKMTILPEKXKHKVKT 208
Db 5 KEEELKGLQYLDYDFQNNQLVIGIQAELPALD-MGGTSDPYVKVFLLPDKKKKPEF 63
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; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-049A-17
Query Match 13.1%; Score 288; DB 2; Length 138;
Best Local Similarity 46.8%; Pred. No. 1.3e-21;
Matches 59; Conservative 22; Mismatches 45; Indels 0; Gaps 0;

QY 289 GELLISLCYQSTNTNLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKC 348
Db 12 GDICTSLRYVPTAGKLTVCILLEAKNLKMDVGLSDPYVKIHLQMONGKRLKXKKTIVKXK 71

QY 349 TPNVAFNELFVFDIPCEGLDISEVFLVLDSESGSNEVIGQLVLAAGTGEHWKEI 408
Db 72 TLNPFNFESFSEIPFEIQKQVQVVTVLDYDKLGKNEAIGKIFVGSNATGTLRHWSDM 131

QY 409 CDYPRR 414
Db 132 LANPRR 137

RESULT 10
US-09-170-996-17
; Sequence 17, Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,996
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,049
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
US-09-170-996-17
Query Match 13.1%; Score 288; DB 3; Length 138;
Best Local Similarity 46.8%; Pred. No. 1.3e-21;
Matches 59; Conservative 22; Mismatches 45; Indels 0; Gaps 0;

QY 289 GELLISLCYQSTNTNLTVVVLKARHLPKSDVSGLSDPYKVNLYHAKKRISKKTHVKKC 348
Db 12 GDICTSLRYVPTAGKLTVCILLEAKNLKMDVGLSDPYVKIHLQMONGKRLKXKKTIVKXK 71

QY 349 TPNVAFNELFVFDIPCEGLDISEVFLVLDSESGSNEVIGQLVLAAGTGEHWKEI 408
Db 72 TLNPFNFESFSEIPFEIQKQVQVVTVLDYDKLGKNEAIGKIFVGSNATGTLRHWSDM 131

QY 409 CDYPRR 414
Db 132 LANPRR 137

RESULT 11
US-09-036-315-9
; Sequence 9, Application US/09036315
; Patent No. 6218523
; GENERAL INFORMATION:
; APPLICANT: French, Cynthia K.
; APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoto, Karen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,315
; FILING DATE: 06-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/047,811
; FILING DATE: 15-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,246
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 018002-000210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..120
; OTHER INFORMATION: /note= "synaptotagmin "A" internal
; OTHER INFORMATION: repeat (amino acid positions 134-254) "
US-09-036-315-9
Query Match 12.3%; Score 271; DB 3; Length 120;
Best Local Similarity 45.3%; Pred. No. 5.5e-20;
Matches 53; Conservative 29; Mismatches 33; Indels 2; Gaps 2;

QY 149 EQEKLGITLFFSLEYNFERKAFVNTKEARGLPAMDEQSWTSIDYIKMTILPEKXKHKVKT 208
Db 5 KEEELKGLQYLDYDFQNNQLVIGIQAELPALD-MGGTSDPYVKVFLLPDKKKKPEF 63
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,049A
; APPLICATION NUMBER: US/08/609,049A
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-049A-16

Query Match      8.3%; Score 182.5; DB 2; Length 140;
Best Local Similarity 32.8%; Pred No. 8.2e-11;
Matches 39; Conservative 29; Mismatches 48; Indels 3; Gaps 2;

QY 154 LGTLFFSLYVNFERKAFVYVNIKEARGLPAMDQSQMTSDPYIKWTILP--EKKHKVKTIVL 211
Db 11 LGALEFSLLYDQDSSSLHCTTIKAKGLKPMDSNGL-ADPYVKLHLPLPGASKSNKLRKTIL 69

QY 212 RKTLDPAPDEFTFYGIPTQIOELALHFTIISLFDPSRDDIIGEVLLPLSGIELSEK 270
Db 70 RNTRNPIWNETLVYHGITDEDMQKTLRISVCDKDFGHNFEIGETFRFSLKCLKPNQK 128

Search completed: February 20, 2004, 13:15:17
Job time : 22 secs
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RESULT 15

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US-09-170-996-16
; Sequence 16, Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,996
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,049
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
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OM protein - protein search, using sw model

Run on: February 20, 2004, 13:06:49 ; Search time 46 Seconds
(without alignments)
1466.496 Million cell updates/sec

Title: US-09-680-121C-2

Perfect score: 2201

Sequence: 1 MAPIITSRREFDELPVTVG.....KEICDPRQRIAKMHLVDG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2201	100.0	425	19 AAW74584	Repro-PC-1.0 prost
2	2201	100.0	425	19 AAW75782	Hormone-regulated
3	1162	52.8	431	22 AAW93420	Human polypeptide,
4	1162	52.8	431	22 AAM39577	Human polypeptide
5	1162	52.8	431	23 AAE17500	Human secretion an
6	1159	52.7	431	22 AAB92921	Human protein sequ
7	1154	52.4	486	22 AAM41363	Human polypeptide
8	757	34.4	474	22 ABB59179	Drosophila melanog
9	622.5	28.3	403	23 ABG70275	Human Synaptotagmi

10	622.5	28.3	474	22	ABB59660	Drosophila melanog
11	614	27.9	195	22	AAU87254	Novel central nerv
12	609	27.7	418	23	ABP69320	Human polypeptide
13	609	27.7	523	23	ABJ04645	Protein of NCVX 6
14	609	27.7	533	23	AAO19183	Human neurotransmi
15	607.5	27.6	1295	22	ABG06581	Novel human diagno
16	603.5	27.4	422	17	AAU87722	Mouse inositol pol
17	603	27.4	188	22	AAU87554	Novel central nerv
18	603	27.4	188	22	AAU19718	Human novel extrac
19	603	27.4	188	22	ABP47938	Human polypeptide
20	603	27.4	425	23	ABP69319	Human polypeptide
21	603	27.4	461	22	AAU19715	Human novel extrac
22	603	27.4	461	23	ABP47935	Human polypeptide
23	586.5	26.6	280	22	ABB59077	Drosophila melanog
24	581	26.4	906	23	ABB08635	GFP fusion protein
25	571.5	26.0	371	23	ABG70274	Human Synaptotagmi
26	568.5	25.8	389	23	ABB97511	Novel human protei
27	518.5	23.6	590	23	ABB05693	Human cell signal
28	518.5	23.6	590	23	AAE17499	Human secretion an
29	507.5	23.1	295	22	AAU19714	Human novel extrac
30	507.5	23.1	295	23	ABP47934	Human polypeptide
31	464.5	21.1	474	21	AAAB41973	Human polypeptide
32	464.5	21.1	474	22	AAAM40253	Human polypeptide
33	464.5	21.1	507	22	AAAM42039	Human polypeptide
34	447	20.3	413	24	ABR39434	Human GENSET polyp
35	428	19.4	412	18	AAW25032	Human Doc2-beta co
36	418	19.0	412	22	AAU87165	Novel central nerv
37	408	18.5	704	15	AAAS7421	Rabphilin-3A. Hom
38	405.5	18.4	361	23	ABU65212	Human NOVI25a prot
39	405.5	18.4	361	23	ABU65213	Human NOVI25a prot
40	395.5	18.0	373	22	AAU87252	Novel central nerv
41	395.5	18.0	375	22	AAU87380	Novel central nerv
42	393.5	17.9	405	20	AAU27275	Mouse Doc2alpha pr
43	384.5	17.5	400	17	AAW01114	Brain-specific pro
44	384.5	17.5	400	20	AAW83429	Human Doc2-alpha.
45	383	17.4	602	22	ABB71195	Drosophila melanog

ALIGNMENTS

RESULT 1
AAW74584
ID AAW74584 standard; Protein; 425 AA.
AC AAW74584;
XX
XX
XX
DT 11-JAN-1999 (first entry)
XX
DE Repro-PC-1.0 prostate cancer-specific marker.
XX
KW Repro-PC-1.0; prostate cancer; marker; synaptotagmin; human;
KW diagnosis; vaccine; therapy.
XX
XX Homo sapiens.
XX
XX PN WC9839447-A1.
XX
XX PD 11-SEP-1998.
XX
XX PF 06-MAR-1998; 98WO-US04488.
XX
XX PR 15-MAY-1997; 97US-0047811.
XX
XX PR 07-MAR-1997; 97US-0041246.
XX
XX (REPR-) REPROGEN INC.
XX
XX French CK, Schneider PA, Yamamoto KK;
XX
XX WPI; 1998-506363/43.
XX
XX DR N-PSDB; AAV54208.
XX
XX New isolated Repro-PC-1.0 polynucleotide(s) - are used to develop

PT products for the detection and prophylactic and therapeutic
 FT treatment of prostate cancer
 XX
 PS Claim 1; Page 68-69; 87pp; English.
 XX
 XX Repro-PC-1.0 is a novel prostate cancer-specific marker, which
 CC represents a novel human brain synaptotagmin isoform that may
 CC function in exocytosis and endocytosis pathways. Its amino acid
 CC sequence was deduced from cDNA clones (see AAV54208) isolated from
 CC a male LNCaP tumour cDNA library. The invention provides
 CC Repro-PC-1.0 polypeptides, fragments and immunogenic peptides
 CC (see also AAW30693-98) capable of inducing a Class I MHC-restricted
 CC cytotoxic T-lymphocyte response or a Class II MHC-restricted
 CC immune response against cells expressing Repro-PC-1.0. Also
 CC claimed are Repro-PC-1.0 polypeptide analogues that act as decoys,
 CC antibodies specific for Repro-PC-1.0, and methods for detecting
 CC Repro-PC-1.0 polypeptide in a sample, for diagnosis of prostate
 CC cancer (by detecting Repro-PC-1.0 mRNA or polypeptide in a sample),
 CC for detecting prostate cancer cells (e.g. using the antibodies of
 CC the invention), for following the progress of prostate cancer, for
 CC treatment of prostate cancer (e.g. using a Repro-PC-1.0 decoy
 CC polypeptide), and a polypeptide vaccine for eliciting an immune
 CC response against Repro-PC-1.0.
 XX
 XX Sequence 425 AA;

Query Match 100.0%; Score 2201; DB 19; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.2e-196;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPKYFVHLKGV 60
 Db 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPKYFVHLKGV 60
 Qy 61 DIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 Db 61 DIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 Qy 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNFERKAFVNNKEARGL 180
 Db 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNFERKAFVNNKEARGL 180
 Qy 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240
 Db 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240
 Qy 241 TILSPDRSRDDIIGEVLPISGIELSEGKMLNREIKNVKSSGRGELLISLCYQST 300
 Db 241 TILSPDRSRDDIIGEVLPISGIELSEGKMLNREIKNVKSSGRGELLISLCYQST 300
 Qy 301 TNLTVVVLKARHLPKSDVSGLSDPVVKVNLHYAKKRIKKKTHVKKCTPNAVFNELVF 360
 Db 301 TNLTVVVLKARHLPKSDVSGLSDPVVKVNLHYAKKRIKKKTHVKKCTPNAVFNELVF 360
 Qy 361 DIPCEGLEDISVEFLVLDSEGRNREIVIGQLVGLAAAGTGGHWEKICDYPKQIAKWH 420
 Db 361 DIPCEGLEDISVEFLVLDSEGRNREIVIGQLVGLAAAGTGGHWEKICDYPKQIAKWH 420
 Qy 421 VLCDG 425
 Db 421 VLCDG 425

RESULT 2
 AAW5782
 ID AAW5782 standard; Protein; 425 AA.
 XX
 AC AAW5782;

DT 21-DEC-1998 (first entry)
 DE Hormone-regulated Repro-PC-1.0 polypeptide.
 XX

KW Repro-PC-1.0; prostate cancer; LNCaP; hormone-regulated gene;
 XX human; synaptotagmin.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 150..252
 FT /note= "repeat region"
 FT Region 276..396
 FT /note= "repeat region"
 FT Domain 15..37
 FT /note= "putative transmembrane domain"
 XX
 PN WO9839661-A1.
 XX
 XX 11-SEP-1998.
 XX
 XX 06-MAR-1998; 98WO-US04519.
 XX
 XX 15-MAY-1997; 97US-0047811.
 PR 07-MAR-1997; 97US-0041246.
 XX
 XX (REPR-) REPROGEN INC.
 XX
 XX French CK, Yamamoto KK;
 PI
 XX
 XX WPI; 1998-506379/43.
 DR N-PSDB; AAV57327.
 XX
 FT Identification of hormone-regulated traits, e.g. in cancers - by
 PT exposing grafts of biological material to different hormonal
 PT environments in animals of different reproductive states
 XX
 XX Example 1; Page 59-60; 85pp; English.
 XX
 CC This polypeptide is encoded by a newly isolated hormone-regulated
 CC gene, termed Repro-PC-1.0 (see AAV57327), isolated from prostate
 CC cancer cells. The polypeptide (calculated mol.wt. 48,070, pI 8.83)
 CC contains 2 copies of a 116-amino acid repeat that show homology
 CC to the C2 regulatory domain of calcium-dependent isoforms of
 CC protein kinase C, and to isoforms of synaptotagmin. Repro-PC1.0
 CC expression is specifically and differentially up-regulated in
 CC LNCaP tumour cells. The invention provides methods of identifying
 CC hormone-regulated traits in a cell. The methods involve
 CC cultivating the cell as a graft in 2 different hormonal
 CC environments and determining whether expression of the trait
 CC differs in the 2 grafts. The methods can be used to identify
 CC hormonally-regulated traits and hormonally-regulated genes for use
 CC as targets for therapeutic intervention in disease states,
 CC particularly cancers.

XX Sequence 425 AA;
 SQ
 Query Match 100.0%; Score 2201; DB 19; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.2e-196;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPKYFVHLKGV 60
 Db 1 MAPITTSREDFEIPVVGIFSAFGLVFTVSLPAWICCCQKSSKSNKTPPKYFVHLKGV 60
 Qy 61 DIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 Db 61 DIYPENLNSKKKFGADDDKNEVKNKPAVPKNSLHLDLEKRDINGNFPKTNLKPSPSDLEN 120
 Qy 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNFERKAFVNNKEARGL 180
 Db 121 ATPKLFLEGEKESVSPESLKSSTLSLSEKQKGLTLPFSLFYNFERKAFVNNKEARGL 180
 Qy 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240
 Db 181 PAMDEQSMSTSDPYIKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALHF 240

QY 241 TTLSDFRFRDDIIGVLPISGIELSEKMLMREIIKRNVRKSSGRGELLISLCYOST 300
 DB 241 TTLSDFRFRDDIIGVLPISGIELSEKMLMREIIKRNVRKSSGRGELLISLCYOST 300
 QY 301 TNLTVVVLKARHLPKSDVSGLDPPYKVNLYHAKKRIKSKKTHVKKCTPNAVFNELFVF 360
 DB 301 TNLTVVVLKARHLPKSDVSGLDPPYKVNLYHAKKRIKSKKTHVKKCTPNAVFNELFVF 360
 QY 361 DIPCEGLEDISVEFLVLDSDRGRNEVIGQVLGAAAGTGGEHWKETCDYPRRQIAKWH 420
 DB 361 DIPCEGLEDISVEFLVLDSDRGRNEVIGQVLGAAAGTGGEHWKETCDYPRRQIAKWH 420
 QY 421 VLCDG 425
 DB 421 VLCDG 425

RESULT 3
 ID AAM93420
 ID AAM93420 standard; Protein; 431 AA.
 AC AAM93420;
 DT 06-NOV-2001 (first entry)
 XX Human polypeptide, SEQ ID NO: 3040.
 XX Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX Homo sapiens.
 XX EP1130094-A2.
 PD 05-SEP-2001.
 XX 07-JUL-2000; 2000EP-0114089.
 XX 08-JUL-1999; 99JP-0194486.
 XX 11-JAN-2000; 2000JP-0118774.
 XX 02-MAY-2000; 2000JP-0183765.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 XX Wakamatsu A, Sugiyama I, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 XX N-PSDB; AAK94341.

PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX Claim 8; SEQ ID NO 3040; 1380pp + sequence listing; English.
 XX The invention relates to primers for synthesising full length cDNA
 XX clones. 830 cDNA molecules encoding a human protein have been
 XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 XX molecules have been determined. Primers for synthesising the full length
 XX cDNA are useful for clarifying the function of the protein encoded by
 XX the cDNA. The full length clones were obtained by construction of full
 XX length enriched cDNA libraries that were synthesised by the oligo-capping
 XX method. The primers enable the production of the full length cDNA easily
 XX without any special methods. The present sequence is a polypeptide
 XX encoded by a full length human cDNA of the invention.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 431 AA;

Query Match 52.8%; Score 1162; DB 22; Length 431;

Best Local Similarity 52.4%; Pred. No. 2.8e-99; Indels 20; Gaps 7;
 Matches 229; Conservative 77; Mismatches 111;

QY 1 MABITTSREEFDEIPTVVGIFSAFLVTVS--LFAWICCCQKSSKSNKTPPYKFEVHLK 58
 DB 1 MABITTNIRPSFDFSPVVGAGLIGASVLYVVCVSVTVFVWSCCHQQAERKKHNPYPKFLHMLK 60
 QY 59 GVDIYENLNKKKF-----GADDKNEVKNKPAVPKNSIHLDLEKRDNLNGNFKTNLKP 113
 DB 61 GISIYETLSNKKKI IKVRRDKDGPREGGRNLLVDAEAGLLSRD-----KDPRGPS 114
 QY 114 SPSDLNATPKL-----FLEGEKESVSPESLSKSTSLTSEEKQELGTLPFSLEYNFERKA 169
 DB 115 SGSCIDQLPIKMDYGEELRSPITSITPGESK-TTSPSPSPEDVMLGSLTFSVDYNFPKA 173
 QY 170 FVNIKEARGLPAMDQSMTPDPYIKMTILPEKKHKVKTIVLRKTLDPAFDETFTYGIP 229
 DB 174 LVVTIQEAHGLPVMDQDQTSQSDPYIKMTILPKRHRVKTIVLRKTLDPVDFDETFTYGIP 233
 QY 230 YTOIELALHFTILSDFRFRSDDIIGEVLIPLSGIELSEKMLMREIIKRNVRKSSGRG 289
 DB 234 YSOQLDLVHLFLVLSDFRFRSDDVIGEVVPLGVDPSTGKVLQTRDIIKRNIOKISRG 293
 QY 290 ELLISLCYQSTTNTLTIVVVLKARHLPKSDVSGLS--DPYKVNLYHAKKRIKSKKTHVKK 348
 DB 294 ELQVSLSYQFVAQRMTVVVLKARHLPKMDITGLSGNPYKVNLYHAKKRIKSKKTHVKK 353
 QY 349 TPNVFNELFVDIPCEGLEDISVEFLVLDSDRGRNEVIGQVLGAAAGTGGEHWKE 407
 DB 354 TLPNPFNESFIYDIPDTLLPDISTIEFLVIDFDRTTKNEVVGRLILGAHVSVTASGAHWRE 413
 QY 408 ICYPRRQIAKWHVLC 424
 DB 414 VCESPRKPAKWHSLSE 430

RESULT 4
 ID AAM39577
 ID AAM39577 standard; Protein; 431 AA.
 AC AAM39577;
 DT 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 2722.
 XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 XX peripheral nervous system; neuropathy; central nervous system; CNS;
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 XX leukaemia.
 XX Homo sapiens.
 XX WO200153312-A1.
 XX 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX 09-JUL-2000; 2000US-0598042.
 XX 19-JUL-2000; 2000US-0620312.
 XX 03-AUG-2000; 2000US-0653450.
 XX 14-SEP-2000; 2000US-0662191.
 XX 19-OCT-2000; 2000US-0693036.
 XX 23-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.
DR N-PSDB; AAI58733.
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX Example 4; SEQ ID NO 2722; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAI42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX
SQ Sequence 431 AA;
Query Match 52.8%; Score 1162; DB 22; Length 431;
Best Local Similarity 52.4%; Pred. No. 2.8e-99;
Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;
Qy 1 MAPITTSREDFEIPTVVGIFSAFGLVFTVS--LFAMICCCQKSSKNKTPPYKFVHLK 58
Db 1 MAEITNIRPSFVSPVAGLIGASVLVVCVTVFVWSCCHCQQAQKKNPPYKFVHLK 60
Qy 59 GVDIYPENLNSKKF-----GADDKNEVKNKPAVPKNSHLHLEKRLDNGNFPKTNLKP 113
Db 61 GISIYPETLSNKKTIKVRDDKDGPGREGRRLLVDAEAGLLSRD-----KDPGRPS 114
Qy 114 SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEKQELGLTFLFSLEYNPERKA 169
Db 115 SGSCIDQPIKNDYGEELKSPITSPFGESK-TTSPSPDEEDVLMGSLTFSVDYNFPKA 173
Qy 170 FVNIKEARGLPAMDEQSMTPYIKWTILPEKKHKVKTALVRLKTLDPADFETTFYGP 229
Db 174 LVVTIOEAGLPVDDOTGSPYIKWTILPDKRHRVKVRLKTLDPVDFETTFYGP 233
Qy 230 YTOIQLALHFTILSFRPSRDDIIGEVJPLSGIELSEKGLMLNREIIKRNVRKSSGRG 289
Db 234 YSQLQDLVLHFLVLSFRPSRDDVIGEVVPLAGVDPSTCKVQLTRDIKRNICKISRG 293
Qy 290 ELLISLCYQSTNTTLTVVVLKARHLPKSDVSGLS-DPYVKVNLVHAKRKISKKTHVKK 348
Db 294 ELQVSLSPQVQRMVTVVVLKARHLPKMDITGSGNPFYVKNVYVYGRKRIAKKTHVKK 353
Qy 349 TPNVFNELFVDPIDCEGELEDISVRFVLDSRGSNEVIGQLVLGA-AAEGTGGEHWKE 407
Db 354 TLNPLFNESFYDIPDLPLDISIEFLFDVDFDRTKNEVGRVLLGAHVSATGAHWRE 413
Qy 408 ICIDYPRRQIAKHVLCID 424
Db 414 VCESRKPQVAKHSLSE 430
RESULT 5
ID AAEI17500
XX AAEI17500 standard; Protein; 431 AA.
AC AAEI17500;
XX
DT 22-APR-2002 (first entry)
XX Human secretion and trafficking protein-9 (SAT-9).

XX Human; secretion and trafficking protein-9; vesicle trafficking disorder;
KW SAT-9; cystic fibrosis; diabetes mellitus; gastrointestinal disorder;
KW Grave's disease; ulcerative colitis; cardiac disorder; hypertension;
KW polymyositis; neurological disorder; Alzheimer's disease; dementia;
KW depression; epilepsy; Tourette's disorder; cell proliferative disorder;
KW cirrhosis; cancer; autoimmune disorder; inflammatory disorder; AIDS;
KW acquired immune deficiency syndrome; Addison's disease; allergy; asthma;
KW atherosclerosis; sickle cell anaemia; hyperglycaemia; transgenic animal;
KW gene therapy; hypotensive; neurotropic; neuroprotective; antidepressant;
XX anticonvulsant; neuroleptic; cytostatic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 16..37
FT /label= Transmembrane_domain
FT Domain 158..285
FT /label= C2_domain
FT Domain 287..419
FT /label= C2_domain
XX WO200202610-A2.
XX PD 10-JAN-2002.
XX 28-JUN-2001; 2001WO-US20704.
XX 29-JUN-2000; 2000US-215465P.
PR 10-OCT-2000; 2000US-239384P.
PR 28-NOV-2000; 2000US-253639P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lee EA, Lu Y, Lal P, Tang TY, Yue H, Wallia NK, Baughn MR, Das D;
PI Ramkumar J, Tribouley CM, Lu DM, Hafalia A, Gandhi AR, Xu Y;
PI Bandman O, Elliott VS, Nguyen DB, Burrill JD, Marcus GA;
PI Zingler KA, Yao MG, Gururajan R, Ding L, Warren BA, Thangavelu K;
PI Lee S;
XX WPI; 2002-154727/20.
DR N-PSDB; AAD28154.
XX Novel human secretion and trafficking polypeptide, useful in diagnosis,
PT prevention and treatment of vesicle trafficking, transport,
PT neurological, autoimmune/inflammatory, and cell proliferative disorders
PT
XX Claim 1; Page 120-121; 131pp; English.
XX The present invention relates to human secretion and trafficking (SAT)
CC proteins and their corresponding polynucleotides. SAT DNAs and proteins
CC are useful for diagnosing, treating and preventing vesicle trafficking
CC disorder (e.g. cystic fibrosis, diabetes mellitus, Grave's disease),
CC gastrointestinal disorders (e.g. ulcerative colitis), cardiac disorders
CC associated with transport (e.g. hypertension, polymyositis), neurological
CC disorders associated with transport (e.g. Alzheimer's disease, dementia,
CC depression, epilepsy, Tourette's disorder), cell proliferative disorders
CC (e.g. cirrhosis, cancer), autoimmune or inflammatory disorders (e.g. AIDS
CC (acquired immunodeficiency syndrome), Addison's disease, allergy, asthma,
CC atherosclerosis) and other disorders associated with transport such as
CC sickle cell anaemia and hyperglycaemia. SAT proteins are useful in a
CC number of drug screening techniques and to analyse the proteome of a
CC tissue or cell type. SAT DNAs are useful for creating knockin humanised
CC animals or transgenic animals to model human diseases, in somatic or
CC germline gene therapy, to generate a transcript image of a tissue or
CC cell type, for detecting differences in the chromosomal location due
CC to translocation, inversion, etc., among normal, carrier or affected
CC individuals, and as hybridisation probes for mapping naturally occurring
CC genomic sequences. The present sequence is human SAT-9 protein.
XX Sequence 431 AA;
SQ

Query Match 52.8%; Score 1162; DB 23; Length 431;
 Best Local Similarity 52.4%; Pred. No. 2.8e-99;
 Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

1 MAPITTSREDFEIPVVGIFSAFLVFTVS--LFAMICCCQKSSKSNKTPPKYKVVHLK 58
 1 MAEITNIRPSDFVSPVAGLIGASVLVVCVSVTVFVWSCCHQQAEEKKHNPYKFIHMLK 60
 59 GVDIYPENLNSKKKF-----GADKNEVKNPAVPKNSLHLDLEKRDNGNPPKTNLKP 113
 61 GISIYPETLSNKKKIIKVRDKDQPGREGGRNLLVDAAEAGLLSRD-----KDPGRPS 114
 114 SPSDLENATPKL-----FLEGEKESVSPESLSKSTSLTSEKQEKLTGTFSSLEYNFERKA 169
 115 SGSCIDQLPIKMDYGEELRSPITSLTPGESK-TTSPSSPEEDVMLGSLTFSVDYNPPKKA 173
 170 FVNVIKEARGLPAMDQESMTSDPYIKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGIP 229
 174 LVVTIQEAHGLPVMDQDQGSDDPYIKMTILPKRHRVTRVLRKTLDPVDFDTFTFYGIP 233
 230 YTOIQELALHFTILSFDRFRDIDIIGEVLIPLSGTIELSEKMLMREIIRKRVKSSGRG 289
 234 YSLOQLVLHFLVLSFDRFRDIDVIGVWVPLAGVDPSTGKQVLTDRDIKRNIOKISRG 293
 290 ELLISLCYQSTNTLTVVVLKARHLPKSDVSGLS-DPYVKNVLYHAKKRIKSKKTHVKKC 348
 294 ELQVLSYQPVQAKMTVVLKARHLPKMDITGLSGNPYVKNVYGRKIAKKKTHVKKC 353
 349 TPNAVFNELFVDFIPCEGLEDISVEFLVLDSEGRSRNEVIGQLVLGA-AAEGTGGEHWKE 407
 354 TLNPIFNESFIYDPTDLLPDISIEFLVIDPDRTTKNEVVGRLILGAHVSVTASGAHWRE 413
 408 ICYPRQIAKHWLCLD 424
 414 VCESPRKPAKWHSLSE 430

RESULT 6
 AAB92921 ID AAB92921 standard; Protein; 431 AA.
 AC AAB92921;
 XT 26-JUN-2001 (first entry)
 DE Human protein sequence SEQ ID NO:11567.
 CE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS EP1074617-A2.
 PN 07-FEB-2001.
 PD 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 PA Ora T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -
 XX Claim 8; SEQ ID 11567; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX Sequence 431 AA;
 SQ Query Match 52.7%; Score 1159; DB 22; Length 431;
 Best Local Similarity 52.4%; Pred. No. 5.2e-99;
 Matches 229; Conservative 77; Mismatches 111; Indels 20; Gaps 7;

QY 1 MAPITTSREDFEIPVVGIFSAFLVFTVS--LFAMICCCQKSSKSNKTPPKYKVVHLK 58
 DB 1 MAEITNIRPSDFVSPVAGLIGASVLVVCVSVTVFVWSCCHQQAEEKKHSPPKFIHMLK 60
 QY 59 GVDIYPENLNSKKKF-----GADKNEVKNPAVPKNSLHLDLEKRDNGNPPKTNLKP 113
 DB 61 GISIYPETLSNKKKIIKVRDKDQPGREGGRNLLVDAAEAGLLSRD-----KDPGRPS 114
 QY 114 SPSDLENATPKL-----FLEGEKESVSPESLSKSTSLTSEKQEKLTGTFSSLEYNFERKA 169
 DB 115 SGSCIDQLPIKMDYGEELRSPITSLTPGESK-TTSPSSPEEDVMLGSLTFSVDYNPPKKA 173
 QY 170 FVNVIKEARGLPAMDQESMTSDPYIKMTILPEKKHKVTRVLRKTLDPADFDTFTFYGIP 229
 DB 174 LVVTIQEAHGLPVMDQDQGSDDPYIKMTILPKRHRVTRVLRKTLDPVDFDTFTFYGIP 233
 QY 230 YTOIQELALHFTILSFDRFRDIDIIGEVLIPLSGTIELSEKMLMREIIRKRVKSSGRG 289
 DB 234 YSLOQLVLHFLVLSFDRFRDIDVIGVWVPLAGADPSTGKQVLTDRDIKRNIOKISRG 293
 QY 290 ELLISLCYQSTNTLTVVVLKARHLPKSDVSGLS-DPYVKNVLYHAKKRIKSKKTHVKKC 348
 DB 294 ELQVLSYQPVQAKMTVVLKARHLPKMDITGLSGNPYVKNVYGRKIAKKKTHVKKC 353
 QY 349 TPNAVFNELFVDFIPCEGLEDISVEFLVLDSEGRSRNEVIGQLVLGA-AAEGTGGEHWKE 407
 DB 354 TLNPIFNESFIYDPTDLLPDISIEFLVIDPDRTTKNEVVGRLILGAHVSVTASGAHWRE 413
 QY 408 ICYPRQIAKHWLCLD 424
 DB 414 VCESPRKPAKWHSLSE 430

RESULT 7
 AAM41363 ID AAM41363 standard; Protein; 486 AA.
 XX AAM41363;
 XX 22-OCT-2001 (first entry)
 DT

Sequence 474 AA;
 Query Match 34.4%; Score 757; DB 22; Length 474;
 Best Local Similarity 38.2%; Pred. NO. 1.6e-61;
 Matches 179; Conservative 82; Mismatches 137; Indels 70; Gaps 14;
 14 IPTVVGIFSAFGLVFTVSLFAWLCQ-----RKSSKSNKTPPYKVF----- 54
 16 VFALIGLTA---AVISSVACICARQMLRNKKQSDHASFPPQTRTPAVRSPSQP 71
 55 -HVLKGVDPYIPENLNGKFKGADKNEVKNKPAVPKN-----SLHLDLEKRDING 103
 72 PHYLK---SPSTGCKQKGLLSPMDQOSTPIAQNPKVYSEEGDGAQHAQQ-----NG 124
 104 N-----FPKTLKPGSPDLNATPKLFLGEGEKE-SVSPESLSKSTSLTSEKQKGLTFL 158
 125 NQLTVVDGNGKLSHLNLSHSPVETIANGSVTTITLDDHSLTNGKLTVTQYKGLTIY 184
 159 FSLYNFERKAFVNVNKEARGLPADEQSWT-----SPYIKMTILPEKKH 204
 185 FKRLYLAERNALMVSIRCRGLPKCGSSGTGDIPTGMNGRTQAATDPYVKLQLLPDKQH 244
 205 KVKTRVLRKTLDPAFDETETFYGIPTQIOELALHFTLSPDRESRDDIIGVLIPLSGI 264
 245 KVKTRVVRNRNPVYDEDFYGLNMDLQNMSLHFVILSPDRYSRDDVIGEVVCELTSI 304
 265 E---LSEGRMLMNRITIKRNV-RSSGRGELLISLCYQSTNTTLTVVVKARHLPKSDVS 320
 305 EIGDISKEALSISKEITPRLSKIRAQGRGELLISLCWQPAAGRLTVLLKARNLPRMVT 364
 321 GLSDPYVKNVLYHAKRISKKTHVKCTPNVFNELFVDP-CEG-----LEDISVFL 375
 365 GLADPYVKIYLLNGQRIAKKTHVKRTLSPVNESFAFDIPAAEGAGASLEGVSLM 424
 376 VLDSEGRSNEVIGQLVGA--ABGTGGEHWKECDYPRRQIAKHVL 422
 425 LLDMDRVTKNEVIGLELGGPNSSTALNHNVEVNCSPRQIAEWHKL 472

RESULT 9
 ID ABG70275
 AC ABG70275;
 XT 05-NOV-2002 (first entry)
 DE Human synaptotagmin-like protein #2.
 QW Human; NOVX; pathological condition; NOVX-associated disorder;
 QW Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
 QW pancreatitis; obesity; diabetes; autoimmune disease; infertility;
 QW renal artery stenosis; interstitial nephritis; glomerulonephritis;
 QW polycystic kidney disease; cataract; Alzheimer's disease; cancer;
 QW acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;
 QW congenital heart defect; scleroderma; endometriosis; haemophilia;
 QW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
 QW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
 QW acne; wound; asthma; human disease; calpain; epain; zinc finger;
 QW low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;
 QW serine protease TLSP; mitogen activated protein kinase kinase-2;
 QW glycan-2 precursor; thymosin beta-10.
 QX Homo sapiens.
 QX W0200255702-A2.
 QX 18-JUL-2002.
 QD 26-OCT-2001; 2001WO-US50925.
 QF 26-OCT-2000; 2000US-243320P.
 QP 26-OCT-2000; 2000US-243592P.

26-OCT-2000; 2000US-243642P.
 27-OCT-2000; 2000US-243681P.
 31-OCT-2000; 2000US-243863P.
 01-NOV-2000; 2000US-244433P.
 01-NOV-2000; 2000US-244995P.
 02-NOV-2000; 2000US-245029P.
 02-NOV-2000; 2000US-245293P.
 02-NOV-2000; 2000US-245315P.
 02-NOV-2000; 2000US-245316P.
 19-JAN-2001; 2001US-262994P.
 15-FEB-2001; 2001US-269056P.
 02-MAR-2001; 2001US-272923P.
 15-MAR-2001; 2001US-276565P.
 07-SEP-2001; 2001US-318119P.
 (CURA-) CURAGEN CORP.
 Gangolli EA, Spytek KA, Casman S, Blalock A, Li L;
 Vernet CAM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;
 Malyankar U, Stone D, Millet I, Smithson G, Gunther E, Padigaru M;
 Taupier RJ, Anderson D;
 WPI: 2002-590673/63.
 X-PSDB; ABK51682.
 Isolated NOVX polypeptides and nucleic acid molecules useful for
 treating, preventing, diagnosing and researching pathological
 conditions in humans with a NOVX-associated disorders, e.g. cancer,
 stroke or Alzheimer's disease -
 Claim 1; Page 46; 236pp; English.
 The present invention relates to a new polypeptide that comprises any of
 17 fully defined sequences of 43-990 amino acids given in the
 specification. The NOVX polypeptide, nucleic acid and antibody of the
 invention are useful for treating or preventing a pathological condition
 in humans with a NOVX-associated disorder, e.g. Von Hippel-Lindau
 syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,
 diabetes, autoimmune disease, renal artery stenosis, interstitial
 nephritis, glomerulonephritis, polycystic kidney disease, cataract,
 Alzheimer's disease, acoustic trauma, cancer, infertility,
 cardiomyopathies, atherosclerosis, hypertension, congenital heart
 defects, scleroderma, endometriosis, haemophilia, dementia, stroke,
 Parkinson's disease, Huntington's disease, epilepsy, multiple
 sclerosis, anxiety, pain, leukaemia, hypothyroidism, psoriasis, acne,
 wounds and asthma. They are also useful for the manufacture of a
 medicament for treating a syndrome associated with a human disease,
 specifically a NOVX-associated disorder. They may also be useful in
 therapeutic applications including protein therapy, as small molecule
 drug targets, as antibody targets, as diagnostic and/or prognostic
 markers, in gene therapy, as research tools and in tissue regeneration.
 The present amino acid sequence represents one of the 17 novel proteins
 of the invention.
 Sequence 403 AA;
 Query Match 28.3%; Score 622.5; DB 23; Length 403;
 Best Local Similarity 36.2%; Pred. NO. 4.1e-49;
 Matches 153; Conservative 71; Mismatches 128; Indels 71; Gaps 11;
 27 VFTVSL-----FAWIC--CQKSSKSNKTPPYKFVHLKGVDPYIPENLNSKKFGADD-- 77
 23 IITVSLSVTVVLCGLCHWCQKGLKRYK-----NSLETFTVGPDSG 62
 78 -----KNEVK-----NKPAVPKNSLHLDLEKRDINGNEPKTNLKPSPSPLENATPK 124
 63 RGRSEKAIKLDPAGKAVNTAPVPGQTPHDSRR-----TEPRS-----SVSLVN----- 109
 125 LFLEGEKESVPSLSKSTSLTSEE-----KQKLGTLFFSLEYNFERKAFVNVNKEARG 179
 110 -----SITSEMLMLSPGSEEDAEHGCSSRENIGRIQFSVGNFQESTLTVKIMKAOE 161
 180 LPAMDEQMSDPIYKMTILPEKKHKVTRVLRKTLDPAFDETFTFYGIPTQIOELALH 239

PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PR Rosen CA, Barash SC, Ruben SM;
 PR MPI; 2001-581633/65.
 PR N-PSDB; ABK43584.
 PR
 PR New isolated nucleic acid encoding a protein for diagnosing,
 PR preventing, treating or ameliorating medical conditions and used as
 PR food additives or preservatives -
 PR Claim 9; SEQ ID No 772; 837pp; English.
 PR
 PR The invention describes an isolated nucleic acid molecule (I) encoding a
 PR novel central nervous system protein. (I) and polypeptides (III) encoded
 PR by (I), are used to treat a medical conditions and in diagnosis of a
 PR pathological condition. Disorders which are diagnosed or treated include
 PR autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative

tranquilliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;
anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
metabolic disorder; obesity; infectious disease; Alzheimer's disease;
anorexia; neurodegenerative disorder; Parkinson's disease; obesity;
immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
metabolic syndrome X; wasting disorder; cancer; neurological disorder;
epilepsy; stroke; mental disorder; schizophrenia disorders; goiter;
vesicular transport; cystic fibrosis; gastrointestinal disorder;
diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
multiple sclerosis; rheumatoid arthritis; AIDS; transgenic animal;
gene therapy.

Unidentified.

WO200246409-A2.

13-JUN-2002.

06-DEC-2001; 2001WO-US46586.

06-DEC-2000; 2000US-251660P.

12-DEC-2000; 2000US-255029P.

08-JAN-2001; 2001US-260326P.

24-JAN-2001; 2001US-263800P.

20-FEB-2001; 2001US-269942P.

24-APR-2001; 2001US-286183P.

20-AUG-2001; 2001US-313627P.

12-SEP-2001; 2001US-318712P.

(CURA-) CURAGEN CORP.

Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Mallyankar UM;

Tchernev VT, Vernet CAM, Spytek KA, Shenoy SG, Alsbrook JP;

Edinger S, Peyman JA, Stone DU, Ellerman K, Gangolli EA;

Boldog FL, Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK;

Zerhusen BD;

WPI; 2002-547774/58.

N-PSDB; ABT05458.

Novel isolated polypeptide, designated NOVX, useful for treating or

preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and

metabolic, neurodegenerative, immune and hematopoietic disorders -

Claim 1; Page 53; 421pp; English.

The invention relates to an isolated polypeptide, designated NOVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polynucleotide or an antibody created from the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder, or for treating or preventing a NOVX-associated disorder in a subject, preferably human. The isolated protein, its encoding polynucleotide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorder, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The isolated protein, its encoding polynucleotide or an antibody created from the protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, disorders of vesicular transport such as cystic fibrosis, diabetes mellitus, goiter, gastrointestinal disorders including ulcerative colitis, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NOVX proteins of the invention.

Sequence 523 AA;

Query Match	27.7%;	Score 609;	DB 23;	Length 523;
Best Local Similarity	34.6%;	Pred. No. 1.1e-47;		
Matches 159;	Conservative 73;	Mismatches 155;	Indels 72;	Gaps 16;
QY	20	IFSAGL-VFTVSLFA-WICQKSSKSNKTPPYKVFHVLKGVDIYPENLNS--KKKFGA	75	
DB	60	VVSFCGLLVSLVSVFWKLC-----WPCWKSFPVTSNITLPOSISAPTEVET	110	
QY	76	DKNEVK--NKPAVPKNSLHLDLEKRLNGFP---KTNLK-----PGSP	115	
DB	111	EKKEIKENEKPAV--KAIEPAIKISHTSPDIPAEVQTALKEHLIKHARVQRIEPTSS	168	
QY	116	S-----DLENATPKLFLEGEKES-----VSPSLKSSSTSLTSEKQEK	153	
DB	169	TRHSPRRHLPRQMVSSVDFSMGTEPVLQRGTEVTSIGRIKPELYKOK-SVDSQNQNE	227	
QY	154	----LGTFLFSLEYNFERKAFVNNIKEARGLPADEQSMSTSDPYIKMTILPKKHVKTR	209	
DB	228	DVKICGKLNFTLQDYENELLVVKIIKALDLPADFTG-TSDPVYVMYLLPDRKKKQFTR	286	
QY	210	VLKRTLDPAFDETFYGIPIYTOIQELALHFTILSDFRSDDDIIGEVILPLSGIELSG	269	
DB	287	VHRKTLNPLFDETFQP-PVAYDQLSNRKLFHSVDFDRFSRDMIGEVLID----NLFEV	341	
QY	270	KMLMREIIRKRVN---KSSGRGELLISLCYQSTTNTLTIVVLKARHLPKSDVSLSDP	325	
DB	342	SDLSREATVWKDIHCATTESIDIGEIFSLCYLPTAGMTLTIVIKRNLKAMDITGSSDP	401	
QY	326	YKVNLYHAKRISKKTHVKTCTPNNAFVNFELFVDIPCEGLEDSVFLVLDSEGRSN	385	
DB	402	YKVSILMCEGRRLKRTTKNTLNPNVNEAIIFFIPPENVDQVSLSAVMDYDRVGHN	461	
QY	386	EVIGQVLVGLAAGTGGEHWKEICDYPKQIAKHWLVD 424		
DB	462	EVIGVCRGTGDAEGLGRDHWNEMLAYHRKPTTHWHPLE 500		

RESULT 14

AAO19183

ID AAO19183 standard; protein; 533 AA.

AC AAO19183;

DT 27-NOV-2002 (first entry)

XX Human neurotransmission-associated protein NTRAN6.

XX Human; neurotransmission-associated protein; NTRAN; autoimmune disorder;
inflammatory disorder; cancer; cardiovascular disorder; infection;
neurological disorder; metabolic disorder; immunomodulatory; nootropic;
neuroprotective; antiinflammatory; cytostatic; cardiant; gene therapy.

OS Homo sapiens.

XX WO200266646-A2.

PN 29-AUG-2002.

XX 15-FEB-2002; 2002WO-US04536.

XX 16-FEB-2001; 2001US-269748P.

PR 11-MAY-2001; 2001US-290524P.

PR 19-OCT-2001; 2001US-343742P.

XX (INCY-) INCYTE GENOMICS INC.

XX Duggan BM, Honchell CD, Ison CH, Thangavelu K, Lu DAM, Baughn MR;

PI Lal PG, Yue H, Tang YT, Warren BA, Lee EA, Griffin JA;

PI Forsythe IO, Wallia NK;

DR WPI; 2002-674945/72.

DR N-PSDB; AAL49656.

1266 WKSPPGEVKKHWDIARPRQPVQWQL 1293

Search completed: February 20, 2004, 13:12:49
Job time : 48 secs